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# SILAC-based quantitative proteomic analysis of *Drosophila* gastrula stage embryos mutant for fibroblast growth factor signaling

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**Abstract**

Quantitative proteomic analyses in combination with genetics provide powerful tools in developmental cell signaling research. *Drosophila melanogaster* is one of the most widely used genetic models for studying development and disease. Here we combined quantitative proteomics with genetic selection to determine changes in the proteome upon depletion of Heartless (Htl) Fibroblast-Growth Factor (FGF) receptor signaling in *Drosophila* embryos at the gastrula stage. We present a robust, single generation SILAC (stable isotope labeling with amino acids in cell culture) protocol for labeling proteins in early embryos. For the selection of homozygously mutant embryos at the pre-gastrula stage we developed an independent genetic marker. Our analyses detected quantitative changes in the global proteome of *htl* mutant embryos during gastrulation. We identified distinct classes of downregulated and upregulated proteins, and network analyses indicate functionally related groups of proteins in each class. In addition, we identified changes in the abundance of phosphopeptides. In summary, our quantitative proteomic analysis reveals global changes in metabolic, nucleoplasmic, cytoskeletal and transport proteins in *htl* mutant embryos.

## Introduction

Quantitative mass spectrometry-based proteomics have been implemented in studying levels of protein expression and protein modifications in various cell types, tissues and organisms for comparing diverse states, such as age, gender, drug treatments or various disease conditions. In 2002, the SILAC (stable isotope labeling with amino acids in cell culture) method was introduced as a tool for studying functional proteomics on a quantitative global scale[1]. SILAC-based mass spectrometry allows to directly compare populations of cells on the basis of differential signature labeling with stable isotopes. For example, one cell line grown on media containing the naturally predominant occurring amino acid is compared with cells grown on media containing a stable isotope-labeled form of that amino acid [2]. SILAC labeling has also proven successful for global quantitative proteomic comparisons of entire organisms including mammalian model systems[3]. Since then various multicellular model organisms were successfully labeled with stable, non-radioactive isotopes (SILAC or $^{15}N$ labeling) including the plant *Arabidopsis thaliana*, the nematode *Caenorhabditis elegans*, the insect *Drosophila melanogaster* and the mammal *Mus musculus*[4-13].

*Drosophila melanogaster* is one of the most widely studied genetically tractable model organism and has been employed for more than a century to advance our understanding in many areas in biology including genetics, developmental cell biology and signal transduction. Protocols for SILAC or $^{15}N$ labeling of *Drosophila* are based on feeding flies with yeast that has been labeled with stable isotopes[4, 9, 11]. Stable isotope labeling in flies has been used to determine sex-specific differences in the proteome of somatic cells[9], differences in the proteome during ageing[14], and differences in proteomes between adults, larvae and pupae[15, 16]. Recently, a quantitative proteomic study investigated the developmental profile of the *Drosophila*

proteome throughout the life cycle using label-free approaches[15]. Proteome studies in embryos obtained from SILAC flies or using label-free methods also addressed proteome dynamics in early development like changes during the oocyte-to-egg transition (oocyte maturation), and the alterations that occur during the transition of the maternal to the zygotic transcriptional programs (maternal/zygotic transition)[8, 17, 18]. Despite the advances in quantitative proteomics and the plethora of mutations in developmental control genes, changes in the proteome of fly embryos homozygously mutant for a recessive developmental gene have not yet been performed due to technical difficulties in obtaining sufficient material.

In this study, we combined the power of *Drosophila* genetics with SILAC labeling to examine changes in the proteome when a major developmental signaling pathway is absent in the early embryo. The *Drosophila* gastrula stage embryo contains a relatively low cellular complexity, but the cells participate in major morphogenetic movements[19]. Most dramatically, the prospective mesoderm germ layer moves into the interior of the embryo, and undergoes an epithelial-to-mesenchymal transition (EMT), and collective cell migration. The latter two morphogenetic events are controlled by the activation of a fibroblast growth factor (FGF) receptor encoded by the *heartless* (*htl*) gene [20-26]. We employed *htl* loss-of-function mutations to investigate the effects of FGF receptor signaling in the context of an entire embryo. The response of mesoderm cells upon Htl receptor activation is rapid as the cells form protrusions and move towards the underlying ectoderm within the range of minutes [27]. Therefore, it has been suggested that initially the Htl signal affects posttranslational modifications and the turnover of proteins involved in cell movements rather than transcriptional responses [27, 28].

One major problem that has hampered the comparative analyses of proteomes from wild-type and mutant embryos was the selection of the homozygously mutant embryos, which make only 25% of the progeny from heterozygous parental animals. A possible solution to this problem would be provided by an independent phenotypic selection marker that can be readily dected early in development, ideally before the gene under investigation becomes active and its mutant phenotype becomes visible. Furthermore, the marker should not affect the viability of the embryo or the organism. In the present study, we used the *halo* mutation which allows the selection of homozygous mutant embryos in early developmental stages[29]. The *halo* mutation causes a readily visible defect in the transport of lipid droplets in early embryos, but does not affect viability and fertility of the organism [29, 30]. We present a protocol for efficient labeling of *Drosophila* embryos with stable non-radioactive isotopes in a single generation combined with genotyping and staging early embryos to discriminate between homozygous *htl* mutant embryos and *htl* heterozygous embryos. Quantitative global proteomic analysis of *htl* mutant embryos resulted in the discovery of protein networks that were down- or upregulated when compared to control embryos.

## Methods

*Drosophila* strains

Fly stocks were kept under standard conditions. The stock containing the loss of function *halo$^{AJ}$* allele and a stock harboring a transgene with the *halo* genomic locus (*p[halo$^{+}$]*) were gifts of M.A. Welte (Univ. of Rochester, U.S.A.)[31, 32]. We used a chromosome harboring transposase *Δ2,3* under the control of a *hsp70* promoter to mobilize the *p[halo$^{+}$]* transposon insertion in the genome and isolated insertions on the autosomal balancer chromosomes TM3, TM6 and CyO. The loss-of-function *htl$^{AB42}$* allele was maintained over a TM6B, *Hu*, *Tb*, *e*, *p[halo$^{+}$]* balancer chromosome and crossed into a homozygous *halo$^{AJ}$* background.

SILAC labeling of *Saccharomyces cerevisiae*

*Saccharomyces cerevisiae BY4742* colonies were allowed to grow for 2 days at 30°C. A single colony was inoculated into 5 ml DOA (Dropout) – no lysine media (synthetic complete) supplemented with 5 µl of heavy lysine (Lys-8; stock: 30 mg/ml) (L-lysine: 2HCl, U-$^{13}C_6$, 99%; U-$^{15}N_2$, 99%, Cambridge Isotope Laboratories, Inc.). The culture was incubated at 30°C for 24 hours. 5 µl of cell suspension was used to inoculate 5 ml of fresh media containing Lys-8 and was incubated for another 24 hours at 30°C in a shaking incubator. 1 ml of culture was used to inoculate 1 l of DOA media containing Lys-8. Incubation took place for another 24 hours at 30°C in a shaking incubator. 1 ml of the culture was saved for a label check and the remaining culture was pelleted by centrifugation. The yeast pellet was resuspended once in $dH_2O$ and centrifuged; the supernatant was discarded and the Lys-8 – labeled yeast was stored at -80°C. Previous protocols used the lysine auxotrophic *S. cerevisiae* stock *SUB62* [9]. We found that the *SUB62* was insufficiently labeled in a Lys-8 containing medium with an

average global SILAC ratio of 1.4 and below suggesting a maximum of 58.4 % Lys-8 label (Suppl. Mat. S1A,B). *SUB62* strain harbors the point mutation *lys2-801*, which was described as an amber mutation in the *lys2* gene and therefore is, in principle, revertible in particular when grown in large cultures. We found that in 1 l cultures the *SUB62* strain undergoes reversion to a lys prototrophic strain and that this effect appears to be enhanced in the presence of Lys-8 as a source (Suppl. Mat. S1). We therefore utilized the strain *BY4742* that carries the *lys2Δ0* mutation, which is a complete deletion of the *lys2* gene and does not undergo reversions[33]. The labeling effiency with *BY4742* was nearly complete exhibiting a global SILAC ratio of around 15 (Suppl. Mat. S1A,C).

SILAC labeling *of Drosophila melanogaster*

150 embryos were transferred onto a fresh apple juice agar plate supplemented with 300 µl of *BY4742* Lys-8 yeast and enclosed with a fly cage. Larvae were allowed to hatch and to feed on Lys-8 labeled yeast at 25°C. Once the larvae started to penetrate the apple juice agar $dH_2O$ was supplemented according to humidity and evaporation to keep the apple juice agar/yeast mixture soft and moist. Pupae were gently transferred onto a fresh apple juice agar plate supplemented with a drop of *BY4742* Lys-8 yeast as food for the hatching SILAC flies. Control flies of the respective genotype were raised according to the same protocol except for using yeast grown on standard Lys-0 containing media.

Protein extraction from yeast

1 ml of Lys-8 *BY4742* culture was centrifuged, the supernatant was discarded and the yeast pellet was resuspended in 150 µl of 2 M NaOH, 1 M β-mercaptoethanol. 5 volumes of protein extract were supplemented with 1 volume of 20 % trichloracetic acid (TCA) and mixed by inversion. The mixture was incubated on ice for 10 minutes and subsequently centrifuged at 14000 rpm for 4 minutes at 4°C. The supernatant was removed, the pellet was washed with cold acetone and air dried. The pellet was resuspended in 8 M urea, 0.4 M ammonium bicarbonate and used for label check via mass spectrometry.

Embryo collection and protein lysis

The embryos were incubated on an agarose coated petri dish, covered with Halocarbon oil (27S; Sigma/Aldrich) and were staged under a dissection microscope in transmitted light. At the desired stages, embryos were dechorionated in 0.5% sodium hypochlorite solution and collected in microtubes (Protein LoBind tubes, Eppendorf), which were kept on dry ice. For lysis, RIPA buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 % NP40, 0.5 % Sodiumdesoxycholate, 0.1 % SDS) was supplemented with proteinase inhibitors (EDTA-free Protease Inhibitor Cocktail, cOmplete$^{TM}$, Roche) and phosphatase inhibitors (PhosSTOP, Roche). 100 µl of buffer was used for embryo lysis for each individual biological replicate. An equal number of embryos were homogenized with a bio-vortexer and incubated on ice for 20 minutes, followed by centrifugation at 14000 rpm for 10 minutes at 4°C. The supernatant was transferred into a fresh microtube and protein concentration was determined (Peptide and Protein Quantification Kit, LavaPep).

In-gel digestion

For each biological replicate, 40 µg of protein were run on SDS-PAGE (4-12% Bis Tris Nupage gels). Each lane was cut into 5 gel pieces for an in-gel digestion (Fig. 1C), and every individual piece was cut into smaller fragments that were rinsed with 100 µl 100 mM $NH_4HCO_3$ : 100% acetonitrile (ACN) for 10 minutes at room temperature in a shaking incubator. The solution was removed from the gel pieces and the washing step was repeated. 50 µl of 100% ACN were added until gel pieces formed an aggregate and turned white. 50 µl of 100 mM $NH_4CO_3$ were added and incubated at 37°C for 30 minutes, while shaking. The solution was removed, and gel pieces were dried in a vacuum centrifuge. 50 µl of 10 mM DTT were added and incubated at 55°C for 45 minutes. After removing DTT, 50 µl of 50 mM iodoacetamide solution was added and the gel pieces incubated for 30 minutes in the dark at room temperature. After removing the iodoacetamide solution, gel pieces were washed again twice with 100 µl 100 mM $NH_4HCO_3$ : 100% ACN for 10 minutes at room temperature in an shaking incubator. After removing the washing solution, gel pieces were dried in a vacuum centrifuge. In-gel digestion with the Lysyl endopeptidase (Lys-C) was performed overnight according to the manufacturers protocol (Lysyl Endopeptidase, Mass Spectrometry Grade, Fujifilm Wako Pure Chemical Corporation). After digestion, 20 µl of 0.1% trifluoroacetic acid (TFA) and 20 µl 100% ACN were added and the mixture sonicated in an ice water bath for 15 minutes. The supernatant was transferred into a new microtube and 100 µl 30% ACN : 0.1% were added to the gel pieces and sonicated in an ice water bath as before. The supernatant was transferred to previously collected supernatant, and 100 µl 50% ACN : 0.1% TFA were added to the gel pieces and handled as before. Pooled supernatant was finally vacuum centrifuged at 60°C to reduce the volume to approximately 100 µl. The peptides were further

cleaned up with C18 columns using HPLC according to standard protocols (GRE support group University of Dundee, Scotland).

SCX chromatography

The peptide sample was reconstituted in 500 µl SCX loading/wash buffer (10 mM $KH_2PO_4$, 25% ACN, pH 3). SCX columns (Thermo Scientific Hypersep SCX; benzosulfonic acid, 25 mg/ml) were washed twice with 1 ml MilliQ water and were primed twice with 1 ml SCX priming/elution buffer (10 mM $KH_2PO_4$, 25% acetonitrile (ACN), 350 mM KCl, pH 3). The sample was loaded onto the column and pushed through slowly. Loaded columns were washed twice with 500 µl SCX wash buffer. Sample elution was achieved with 500 µl of SCX elution buffer and the eluate was cleaned up by reversed phase chromatography on a C18 column.

Phosphopeptide enrichment by $TiO_2$ binding

The unbound fraction of the SCX chromatography was subjected to phosphopeptide enrichment using affinity binding to $TiO_2$ beads. The $TiO_2$ beads were primed with 2x loading buffer (80% ACN, 2% TFA), 200 mg/ml 2,5-dihydroxy-benzoic acid, pH 2.0). the flow through of the SCX column was reduced to 100 µl by speed vacuum, resuspended in loading buffer and added to primed $TiO_2$ beads. After 1 h incubation at room temperature under agitation, beads were washed three times with 100 µl loading buffer, then washed three times with wash buffer (80% ACN, 2% TFA). Phosphopeptides were eluted from $TiO_2$ beads with 400 mM $NH_4OH$, pH 11.0. The eluate was purified by reversed phase chromatography on a C18 column before analysis by LC-MS/MS.

LC-MS/MS analysis

The peptide samples were run on a Thermo Fischer Orbitrap Velos Pro. They were separated on an Easy-Spray reversed chromatography C18 Column (ES803A, 75 μm, 500 mm). The LC temperature was 30° C, the LC conditions were from 2% B to 95% B over a 120 minute gradient (Solvent A: 0.1% Formic acid; Solvent B 80% ACN, 0.1% Formic acid). The flow rate was 200 nl/min. The fragmentation spectra were acquired at 2 Th precursor isolation width and a normalized collision energy of 35%. The resolution of the first MS run was 60,000 (scanning from 335-1800 m/z) and the top 15 ions selected for MS run 2 with a dynamic exclusion window of 30 seconds.

Data analysis

Raw MS data were analyzed with MaxQuant [34] version 1.5.2.8 and searched against the Uniprot *Drosophila* January 2016 database. The modifications used for L-lysine quantitations were: Lys-0: $^{12}C_6$, 99%; $^{14}N_2$, 99% (MW: 182.65); Lys-8: $^{13}C_6$, 99%; $^{15}N_2$, 99% (MW: 190.59). Default MaxQuant settings were used throughout with variable modifications set as Acetyl (Protein N-term); Oxidation (M); Deamidation (NQ); Gln->pyro-Glu; Phospho (STY) and fixed modifications set to Carbamidomethyl (C). Protein and peptide False Discovery Rate (FDR) cut offs were both set to 0.01, and a minimum peptide length was set to 7 amino acids. Only proteins with >1 peptide coverage were included in further analysis, with reversed and contaminant protein identifications removed. All quantified peptides were specified as the modified and unmodified versions. Statistical analysis was carried out with Perseus[35] and Microsoft Excel. Protein network analyses of down- and upregulated proteins were conducted with STRING version 10.5 (https://string-db.org/) [36]. The settings used for the STRING

analyses were default settings including basic settings in which the network edges indicate the type of interaction evidence, and included text mining, experimental evidence, databases, co-expression, neighborhood, gene fusions or co-occurrence. The color code annotation for the edges is indicated in the figure legends. The minimum required interaction score was set on medium confidence (0.4) and the interactions were tested for the query proteins only. No clustering was applied and no enrichment analysis was performed.

## Results

Generation of large quantities of SILAC flies

The aim of this study was to determine changes in the proteome of tightly staged gastrula embryos that are depleted of signaling through the FGF receptor Htl. The collection of tightly staged homozygous *htl* mutant embryos requires large quantities of heterozygous flies, because only a quarter of the embryos of this fly stock will be homozygous for the mutation. In addition, the time window for collecting the embryos at the gastrula stage only lasts about 15 min. The SILAC fly was described previously using protocols that reared flies on minimal media, e.g. Lys-8 labeled yeast on cotton wool with sucrose or low-melt agarose containing glucose for efficient labeling [9, 11]. In our hands, these procedures did not produce sufficient amounts of healthy flies; larvae developed initially normal and formed pupae, but many flies died before eclosion. In order to obtain healthy populations of SILAC flies that were required for collecting sufficient quantities of staged embryos, we set out to improve the labeling procedure (see methods). In particular, the substitution of low-melting agarose by apple juice agar did not compromise the labeling. This protocol produced large quantities of healthy Lys-8 labeled SILAC flies that produced embryos with >92% labeling efficiency (Fig. 1).

Identification of pre-gastrula stage *htl* mutant embryos

Before gastrulation commences, the *Drosophila* embryo consists of a monolayered epithelium, called blastoderm epithelium, that surrounds a central yolk cell [37, 38]. The mesoderm germ layer originates from the ventral domain of the blastoderm epithelium and is internalized in a process called mesoderm invagination. After invagination, the mesoderm cells spread out in mid gastrulation to form a single

cell layer upon the basal surface of the neuroectoderm epithelium. This morphogenetic event, referred to as mesoderm spreading, is controlled by signaling through the FGF receptor Htl [20, 28]. Embryos heterozygously mutant for *htl* are viable, but homozygous *htl* mutant embryos exhibit severe mesoderm spreading defects and die during late embryogenesis [21-23]. To analyse changes in the proteome that are elicited by Htl FGF receptor signaling during mesoderm spreading, embryos mutant for *htl* should ideally be collected and compared to wild-type embryos at mid gastrula stages. However, it is impossible to discriminate *htl* homozygously mutant embryos from wild type embryos under the dissecting microscope at mid gastrulation, because the *htl* mutant phenotype cannot be identified at these stages. In order to overcome this problem, we made use of the *halo* mutation as an independent genetic selection marker.

Flies mutant for the zygotic locus *halo* are viable and fertile, but homozygous *halo* embryos exhibit a phenotype in the blastoderm embryo that can be readily scored under the dissecting microscope [30,32]. The *halo* gene is required for proper transport of lipid droplets from the periphery of the blastoderm embryo towards the central yolk cell leaving behind a rim of clear cytoplasm (Fig. 2A). In *halo* mutant embryos, clearing of the lipid droplets is blocked and the periphery of the embryo remains opaque due to persisting lipid droplets (Fig. 2B). The *halo* phenotype can be rescued by a transposon insertion containing the genomic *halo* sequence, called *p[halo$^+$]*[31]. We linked the *halo* rescue transgene *p[halo$^+$]* with the wild-type *htl* allele on balancer chromosomes. Balancer chromosomes are used to maintain recessive mutations in such a way that all inbred flies are heterozygous for the mutation and for the balancer chromosome. Thus, in a typical cross of heterozygous *htl* parents, one quarter of the embryos are homozygously mutant for the *htl* mutation and do not carry the balancer chromosome. In a *halo* mutant background, the *htl* mutant embryos will have lost the

*p[halo$^{+}$]* balancer chromosome and therefore represent the only embryos that will show the *halo* phenotype (Fig. 2).

For each experiment, *halo* mutant embryos from the *halo$^{AJ}$ ; htl$^{AB42}$* / TM6 *p[halo$^{+}$]* stock were first selected on the basis of their *halo* phenotype at the cellular blastoderm stage and then aged until mid gastrulation (stages 7/8; Fig.2). At mid gastrulation, the embryos were collected on dry ice to immediately stop development[39] (Fig. 2A',B'). We have chosen this developmental stage for the sampling, because we were interested to identify protein changes that are invovled in Htl-dependent mesoderm spreading [27]. Approximately 100 tightly staged embryos were collected this way to obtain 40 µg of total protein for each biological replicate. Because the *halo* mutation itself could have an effect on the global proteome, we labeled *halo$^{AJ}$* homozygous mutant embryos with Lys-8 as control sample for comparison with *halo$^{AJ}$ ; htl$^{AB42}$* heterozygous embryos. Additionally, we compared Lys-8 labeled *halo$^{AJ}$* embryos with Lys-0 unlabeled *halo$^{AJ}$* embryos to identify false positive candidates, which might be caused by the stable-isotope labeling itself (see below).

SILAC-based quantitative proteomic analysis of *htl* mutants

Flies that were homozygously mutant for *halo$^{AJ}$* were labeled with Lys-8 as described in the methods section. We found that a single generation reared on Lys-8 labeled yeast was sufficient to produce isotope-labeled embryos. Such embryos showed robust incorporation of Lys-8 at a ratio of over 92% (Fig. 1D). The comparison of Lys-8 labeled embryos of *halo$^{AJ}$* mutants with Lys-0 unlabeled *halo* mutant embryos did not show any major changes in protein ratios indicating that the stable isotope labeling itself did not produce false positives (Fig. S2). For quantitative proteomic analysis, we collected late gastrula embryos from a Lys-8 labeled homozygous *halo$^{AJ}$*

; *htl*$^{+}$ stock and Lys-0 labeled homozygous *halo*$^{AJ}$ ; *htl*$^{AB42}$ embryos (Figs. 1,2). The protein lysates were mixed at equal protein concentrations such that 40 µg of total protein was size-separated on SDS-PAGE and digested by Lys C (Fig. 1). The resulting peptides were applied to SCX (strong cation exchange) chromatography for phospho-peptide enrichment. One aliquot in each biological replicate was kept as a reference for unenriched samples (see below). Both samples of each biological replicate were analysed by LC-MS/MS independently.

All experiments together detected a total number of 81.719 peptides including the comparison of the Lys-8 vs. Lys-0 labeled *halo*$^{AJ}$ experiment. Using MaxQuant analysis these peptides were assigned to 2,131 proteins. All raw data and MaxQuant output tables are accessible in the Proteome Xchange repository PRIDE under accession number PXD016438. In between the three experimental replicates of the *htl*$^{AB42}$ homozygous compared to wild-type control embryos 994 proteins were found in all three experiments and therefore were selected for further analysis. Single peptide protein identifications were excluded from our analyses. The average sequence coverage of these proteins was at 24.57% (STDEV: 15.92%). The overall changes in protein abundance was analyzed between embryos derived from *halo* control and *htl* mutant flies. The population histograms showed a positive correlation of the Lys-8 over Lys-0 labeled proteins, hereafter named (H, heavy)/(L, light) ratios, in all three bio replicates. This indicated that the majority of proteins did not significantly change in abundance between control and *htl* mutant embryos (Fig. 3A). The correlations of the three biological replicates with each other was tested in pairs by plotting the Log 2 ratios of heavy to light labeled proteins using Perseus [35]. Scatter plot analyses of the individual replicates to each other confirmed a positive relationship with Pearson

correlation co-efficient values larger than 0.5, indicating a large correlation between the biological replicates (Fig. 3B).

Changes of protein abundance in *htl* mutant embryos

The positive correlation of the replicates provided a basis to determine changes in protein abundance that were consistent in all three experimental repeats. The median and standard deviations of the population distributions were calculated to determine the average cut-off values for up- and downregulated proteins within fold-change range of +/- 1.1. We found that 36 proteins were consistently downregulated in *htl* mutant embryos, whereas 25 proteins were consistently upregulated in all three biological replicates (Table 1, 2). We also detected six significant changes (two upregulated and four downregulated) in protein regulation when comparing Lys-8 labeled *halo* mutant embryos with Lys-0 unlabeled *halo* mutant embryos. These changes were scored to be false positives and were not considered in further analyses (Fig. S2B). The positive correlation between the three biological replicates allowed for the examination of statistically relevant changes in the protein abundances between control and $htl^{AB42}$ mutant embryos. To consider both the degree of fold changes of proteins and the statistical significance (-logP value) of the change, we visualised the data using a Volcano plot (Fig. 4; Table 3).

To determine whether the up- or downregulated proteins shared any functional features, we performed STRING network analyses[36]. These analyses revealed that 31 of the downregulated proteins and 18 of the upregulated proteins were linked and belonged to networks for which STRING found independent evidence for interaction (see Material and Methods section for parameters and settings of STRING analyses). In *htl* mutant embryos the largest class of downregulated proteins was associated with

chromatin (Fig. 5). Other downregulated proteins were found to occur in networks that included intracellular transport, mRNA binding/processing and translation. Interestingly, we found central components of the endomembrane transport machinery, including Clathrin heavy chain, Vps35, and the coatomer component COP1 alpha. In addition, we also found cytoskeletal components like Myosin heavy chain, Tubulin, the microtubule regulator Mini spindles and Dynein heavy chain 64C to be downregulated in *htl*$^{AB42}$ mutant embryos (Table 1). To a smaller extent we detected downregulation of some metabolic and cytoskeletal components in *htl*$^{AB42}$ embryos. In contrast to the downregulated proteins, the largest network detected to be upregulated in *htl*$^{AB42}$ embryos is affecting metabolic pathways. Some proteins affecting chromatin and cytoskeletal networks were additionally found to be upregulated. A small number of proteins could not be assigned to particular networks (Figs. 5,6).

Analysis of Phosphopeptides

The responses of the mesoderm cells upon Htl FGF receptor activation involves the phosphoregulation of proteins in the cytoplasm (Muha and Muller, 2015). Therefore one aim of this study was to determine changes in the phosphorylation pattern of cellular proteins to further understand the mechanisms of how the Htl FGF receptor changes cell behaviors. In order to increase recovery of phosphopeptides we applied strong anion exchange chromatography (SCX) and in addition $TiO_2$ chromatography on the SCX unbound peptides. The SCX chromatography alone revealed a consistent enrichment of phosphopeptides and also exhibited highest level of consistency in between the different bioreplicates. 85% of all the multiply detected phosphopeptides in our experiments were enriched in the SCX fractions and only 3

additional phosphopeptides were detected in the SCX column-unbound fraction using $TiO_2$ affinity binding (Suppl. Mat. S3A,B). These results indicate that the SCX chromatography proved useful for enrichment of phosphopeptides in our experiments.

In total we identified 203 distinct phosphopeptides with phosphosites on Ser, Thr or Tyr in all bioreplicates, including the non-enriched samples (Suppl. Mat. S3A). 131 of these 203 phosphopeptides were single peptide detections and were therefore not considered any further. The remaining 72 phosphopeptides were detected more than once, with 42 phosphopeptides detected in at least two bioreplicates and 12 phosphopeptides detected in all 3 bioreplicates (Suppl. Mat. S3B). 7 of the 12 phosphopeptides that were found in all 3 bioreplicates were detected in the SCX-enriched samples, 3 were detected in the unenriched samples, while 2 were found in $TiO_2$ enriched fractions (Table 4). Among the 12 phosphopeptides found in all three bioreplicates, 9 phosphopeptides exhibited log2 values within a fold-change range of +/- 1.1. This analysis suggested that 8 phosphopeptides were downregulated and one phosphopeptide was upregulated in *htl* mutants (Table 4). The comparison to the heavy/light ratios levels of the respective proteins indicated that the changes in phosphopeptide levels were unlikely to be a consequence of changes in the overall protein levels (Table 4). Interestingly, three of the respective proteins, Garz, Spoon and Amun, are known to be involved in cell signaling[40-42]. One protein, ADF/cofilin encoded by the *twinstar* (*tsr*) gene, is a well characterized regulator of the actin cytoskeleton in cell migration[43]. Therefore we conclude that our experiments revealed candidates involved in Htl-dependent signaling events or might be the targets of such signaling events (Table 4).

## Discussion

Although *Drosophila* is one of the most studied model organisms, it is somewhat surprising that quantitative proteomics have not been applied more extensively for the analyses of embryonic mutants [9, 11, 12]. One possible reason for this might relate to problems in growing healthy populations of flies that have incorporated stable non-radioactive isotopes. Furthermore, since *Drosophila* is routinely labeled with heavy L-lysine, peptides for mass spectrometric analysis are generated by lysyl-endopeptidase treatment. This endopeptidase is mandatory to ensure that all peptides contain at least one labeled amino acid. However, Lys8-labeled peptides are generally larger resulting in reduced sequence coverage compared to tryptic peptides, which arise from cleavage at lysine and arginine sites. Arginine is less useful for stable isotope labeling in *Drosophila*, because flies survive on an arginine deficient diet [44]. A further drawback in stable isotope labeling of amino acids in *Drosophila* is that both lysine and arginine can be metabolized into several other amino acids in the fly and this can affect the quantitation of the heavy and light ratios [16]. The use of lysine and arginine for stable isotope labeling could be improved by applying mutations that affect the metabolic pathways involved in arginine synthesis or pathways that convert lysine and arginine into other amino acids. Successful application of such mutants will allow the combined labeling of lysine and arginine and allow the use of trypsin which will improve the analyses and the quantitiation of the MS/MS data.

In this work, we were able to conduct a global proteomic analysis of embryos depleted for Htl FGF receptor signaling by combining genetics with a modified, more feasible and cost-efficient way of labeling *Drosophila* with stable non-radioactive heavy L-lysine. The SILAC fly was established previously, however unfortunately, we were not able to obtain large enough quantities of flies following these protocols confirming

previous reports indicating growth retardation and low survival rates of larvae by replacing normal fly food with stable isotope labeled yeast [9, 11]. Here, we introduce a protocol that overcomes the decreased fitness of both larvae and flies, and that produces robustly labeled embryos in a single generation. We found that animals raised on apple juice agar supplied with the Lys-8 labeled yeast strain *BY4742,* were eclosing with expected ratios and appeared healthy. Our results suggest that low eclosing rates, as were observed using other protocols, might be due to the minimal food and lack of minerals and/or vitamins. We conclude that our protocol produces robustly labeled embryos while requiring only low amounts of labeled yeast, which together makes the SILAC fly an economically attractive approach.

Since we wanted to monitor the proteomic change in embryos depleted for FGF signaling during gastrulation stages, it was necessary to establish a reliable marker for the selection of embryos homozygous for the mutation in the FGF receptor Htl. Here we established a method using the *halo* mutation as a genetic marker, which is readily visible in transmitted light in living embryos [29]. Linking a transgenic *halo* rescue construct with a balancer chromosome allowed us to select *htl* homozygously mutant embryos before gastrulation by the presence of the *halo* phenotype. Other methods, like linking GFP to balancer chromosomes, do not provide a reliable signal-to-noise ratio for efficient selection in early embryos. *halo* has been previously used for early selection of homozygous mutations, but its use was restricted for genes located on the second chromosome [32]. The establishment of balancers containing the transgenic *p[halo$^{+}$]* in a *halo* mutant background opens the opportunity for the application of this technique to other experiments in order to genotype and select embryos homozygous for zygotic mutations before the actual phenotype occurs.

The *halo* linkage method was employed to collect tightly staged, homozygously *htl* mutant gastrula embryos for quantitative proteome analyses. By LC-MS/MS we compared unlabeled *htl* mutant embryos with stable isotope labeled *halo* embryos as control. Our data indicate that the lack of Htl FGF receptor signaling in the early embryo affects the abundance of proteins involved in the regulation of chromatin, nuclear transport, mRNA function, and endomembrane transport as well as the cytoskeleton. The majority of the upregulated proteins are related to various metabolic pathways including amino acid biosynthesis and carbohydrate metabolism.

As a classic receptor tyrosine kinase (RTK), the Htl FGF-receptor elicits its signaling activity by triggering phosphorylation cascades that transmit the signal by modifying other proteins, carbohydrates and lipids (Muha and Muller, 2015). The only protein previously known to be directly involved in RTK signaling and detected in our experiments was the *Drosophila* homolog of Importin 7, which is encoded by the gene *moleskin* (*msk*)[45]. Msk was previously shown to function in RTK signaling, including EGF signaling and FGF signaling[45], and found to mediate the nuclear transport of activated ERK in the EGF receptor pathway[46]. Our finding that depletion of Htl signaling causes a reduction in the level of Msk suggests that Htl signaling promotes the stabilisation of Msk protein levels. Interestingly, Msk has important functions beyond nuclear transport. A role of Msk in cell adhesion and in the activation of the small GTPase Rac has been reported and is particularly interesting in the light of our previous studies demonstrating a critical role for Rac GTPase signaling in Htl-dependent mesoderm spreading[45, 47, 48].

During gastrulation, Htl signaling is required for the control of the cell behavior in the mesoderm, but the molecular pathways that trigger these cellular changes are not well understood[28]. The proteins, which levels were reduced in embryos lacking Htl

signaling may represent candidates for FGF-dependent signaling events involved in controlling these morphogenetic movements. These Htl-dependent cellular changes require the modification of cell interactions and the cytoskeleton. Consistent with this notion, we found that the levels of tubulin 67A, the microtubule plus-end-binding protein Mini spindles, the cytoplasmic dynein heavy chain 64C and non-muscle myosin heavy chain were all reduced in *htl* mutants. Another interesting group of candidates were proteins involved in intracellular transport including endomembrane transport (Clathrin heavy chain and COP1 alpha). These proteins are components of two distinct pathways. Clathrin mediates transport in the endosomal system, while COP1 alpha is involved in the secretory pathway and in the retrograde transport within the Golgi complex[49]. Binding of FGF ligands to their receptors stimulates Clathrin-dependent receptor endocytosis, which has been considered both as one mechanism of signal attenuation, but also as a mechanism of signal propagation[50]. COP1 alpha may also be indirectly involved in cell motility, as the assembly of the COP1 coatomer requires the small GTPase ARF1, which plays a role in protrusion formation during cell migration[51, 52].

A surprising finding was the reduction in *htl* mutants of proteins involved in nuclear transport (Moleskin, Artemis/Apollo1 [both RanGTP binding proteins], and Nup50). Nuclear transport of signaling proteins may play an important role in signal propagation during cell migration. A key factor in Htl-mediated mesoderm spreading is the Rho-guanine nucleotide exchange factor Pebble (Pbl)[25, 48, 53]. During interphase, Pbl is accumulated in the nucleus and a small amount of Pbl is localized at the cytocortex, where it is required to activate the small GTPase Rac for proper mesoderm spreading[25, 48]. We previously found that Pbl acts downstream of Htl, but the mechanism of this regulation by Htl is not understood[25]. One possibility would be that

Htl controls the nuclear transport or nuclear retainment of Pbl through components of the nuclear transport machinery. It will therefore be interesting to determine whether FGF signaling impacts on nuclear transport.

One initial aim of this study was to determine changes in the phosphorylation pattern of cellular proteins. However, the identification of phosphopeptides proved to be rather inefficient in our experimental setup, probably due to the low amount of peptides that could be applied to enrichment of phosphopeptides for SCX and $TiO_2$ chromatography. A single embryo only contains around 1 µg of protein, which requires to collect a large number of staged embryos for quantitative proteome analyses. To extend the global proteomic analysis of FGF receptor-depleted embryos towards the phosphoproteome will require the scaling up of each biological replicate by a factor of 20 in order to obtain enough material for enrichment of phosphopeptides using $TiO_2$ or Ti-IMAC [54, 55]. Alternatively, large-scale quantification of phosphorylated peptides can be also combined by the spike-in SILAC method [56, 57]. Nevertheless, the limited data of our phosphopeptide analyses suggested that in principle changes in interesting candidates in signaling events can be identified. Our detection of the reduced level of Serine 3 phosphorylation of Tsr, the *Drosophila* homolog of ADF/cofilin can be regarded as a proof of concept. Ser 3 phosphorylation of ADF/cofilin plays a evolutionary conserved role in the regulation of ADF/Cofilin during directional cell migration[58]. Strikingly, the phosphorylation of Ser 3 is dependent on Rac GTPase signaling downstream to PAK that phosphorylates LIM-Kinase, which in turn phosphorylates ADF/Cofilin on Ser 3 to promote F-actin remodelling [59]. Our discovery of changes in Tsr phosphorylation provides an excellent candidate pathway acting downstream of the Pbl/Rac GTPase activation downstream of the FGF receptor.

The discovery of changes in amounts of interesting proteins that fall into functionally related classes and changes in the levels of a limited number of phosphosites, represents a starting point for further functional analyses. The most important issue will be to determine the tissue-specificity of potential protein functions in Htl FGF receptor induced responses. *Drosophila* provides a rich resource to tackle this problem, for example by tissue-specific RNAi-mediated gene knock-down[60], expression of phosphosite mutant variants or tissue-specific protein knock-down[61].

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**Figures legends:**

**Figure 1: SILAC workflow using *Drosophila* embryos**

(A) *Drosophila melanogaster* flies were grown on media containing Lys-0 or Lys-8 labeled yeast, respectively, and embryos were collected in microtubes on dry ice. After embryo lysis equal amounts of protein were mixed and separated via SDS-PAGE. Then 'in-gel' digestions with Lys C endopeptidase were performed using 5 different SDS PAGE Gel slices per sample (indicated by red lines in C). The major fraction of the resulting peptides were applied to an SCX column. In addition, aliquots were kept before SCX enrichment as a reference. The SCX flow through was subjected to $TiO_2$ chromatography. The SCX fractions, $TiO_2$-bound peptides and the unenriched samples were run on a *LC-MS/MS Velo Orbitrap* instrument and data analyses were carried out using MaxQuant and Perseus. **(B)** *Drosophila* embryos were genotyped in cellular blastoderm stages as described below (see Fig. 2) and collected in mid-gastrula stages (early stage 8; anterior is left, dorsal up). **(C)** The 3 biological replicates (B1-B3) and a Lys-8 $halo^{AJ-/-}$ / Lys-0 $halo^{AJ-/-}$ comparison are shown after SDS-PAGE and Coomassie staining. Red lines indicate separation of the sample lines for further preparation. **(D)** Rearing $halo^{AJ}$ embryos on Lys-8 containing yeast leads to heavy flies that produce embryos with a Lys-8 incorporation of > 92%.

**Figure 2: *halo* as a selection marker for the identification of *htl* mutant embryos**

Brightfield images of living embryos from the inbred line $w^{1118}$ ; $halo^{AJ}/halo^{AJ}$ ; $htl^{AB42}$,*e*/*Tm6*,*e*,*Hu*,*Tb*, p[$halo^{+}$]. The *halo* gene is located on the second chromosome and the *htl* gene is located on the third chromosome. The genomic region containing the *halo* gene was inserted onto the Tm6 balancer chromosome. (**A**) Embryo at the

cellular blastoderm stage exhibits a rim of clear cytoplasm due to clearing of lipid droplets. (**B**) Embryos mutant for *halo*$^{AJ}$ develop an opaque ring in cellular blastoderm stages due to defect in clearing of lipid droplets. (**A**) The *halo*$^{AJ}$ mutant phenotype is fully rescued by the TM6 *p[halo*$^{+}$*]* balancer chromosome. *htl*$^{AB42}$ embryos were therefore identified by the *halo*$^{AJ}$ phenotype, which indicates the absence of the balancer chromosome. The *halo* phenotype is only detectable during stage 5 of embryogenesis and disappears once gastrulation has started (**B'**). Homozygous *halo* mutant embryos were selected at cellular blastoderm stages and transferred to a fresh apple juice plate on which they were aged to mid gastrulation (stage 7/8) (A',B') and then frozen on dry ice.

**Figure 3: Population statistics of *htl*$^{AB42}$ embryos**

**(A)** The distribution of the Lys-8 (H) over Lys-0 (L) protein ratios were found to be centered around 0 in all three biological replicates. The upper panel shows H/L ratios of unenriched sample sets (from aliquots taken before SCX enrichment) and the lower panel H/L ratios after the respective SCX chromatography. H/L protein ratios represent normalized values. **(B)** Scatter plots to indicate the correlation of the individual biological replicates to each other with Pearson correlation co-efficients larger than 0.5. The scatter plots on the left hand side represent the correlation of the unenriched data sets (before SCX chromatography); the right hand panels show the correlation between the bioreplicates after SCX enrichment. The fine lines within the scatter plots indicate the position of the perfect XY distribution of the two populations.

**Figure 4: Changes in the proteome of Htl receptor deficient embryos**

Vulcano plot depicting the quantification of proteome changes of *htl* mutant embryos during gastrulation. Relative fold changes are depicted as log2 averaged SILAC ratios of all three biological replicates and were plotted against the -log10 t-test p-value. Up- and downregulated proteins are indicated with cut-offs +/-1. One particular candidate (Q9VDT1, Arc42) was also identified as downregulated when comparing Lys-8 *halo* vs. Lys-0 *halo* mutants and thus considered as false positive.

**Figure 5: String analysis of downregulated proteins**

Summary view of the network of downregulated proteins in embryos lacking the Htl signaling pathway during gastrulation. The network analysis indicates the downregulation of proteins that are associated with chromatin, nuclear transport, the binding or processing of mRNA, and translation. Central components of the cytoskeleton, such as Myosin heavy chain, Tubulin, the microtubule regulating protein Mini spindles and Dynein heavy chain 64C, are also downregulated when Htl FGF signaling is depleted. A few downregulated components belong to metabolic and cytoskeletal pathways but could not be assigned to any particular network in *htl* mutant embryos. The connecting lines indicate the source of evidence for the interactions in the following color code: known interactions: turquoise - from curated databases, - magenta - experimentally determined; predicted interactions: green - gene neighborhood, red - gene fusions, blue - gene co-occurrence; others: yellow green - textmining, black - co-expression, purple - protein homology.

**Figure 6: String analysis of upregulated proteins**

Summary view depicting the network of upregulated proteins in embryos lacking Htl FGF signaling. Most of the identified upregulated proteins were assigned to metabolic pathways, whereas some proteins belong to chromatin and cytoskeletal networks. A few candidates were not assigned to any particular network. The connecting lines indicate the source of evidence for the interactions in the following color code: known interactions: turquoise - from curated databases, - magenta - experimentally determined; predicted interactions: green - gene neighborhood, red - gene fusions, blue - gene co-occurrence; others: yellow green - textmining, black - co-expression, purple - protein homology.

**Supplemental Material:**

**Suppl. Mat. S1: Incorporation of Lys-8 in yeast *SUB62 vs. BY4742* strains**

(**A,B**) Label check on *SUB62* grown in 1l Lys-8 containing culture. Global peptide ratios (**A**) and representative spectra (**B**) from *SUB62* grown to saturation in 1l Lys-8 culture. An average global SILAC ratio **(A)** of 0.980 indicates incomplete SILAC labeling of *SUB62*. (**B**) representative spectra of FALGQGVGVILCIGETLEEK peptide from Triosephosphate isomerase, with a calculated SILAC ratio of 1.110. (**A,C**) Label check on *BY4742* grown in 1l Lys-8 culture. Global peptide ratios (**A**) and representative spectra (**C**) from *BY4742* grown to saturation in 1l culture supplemented with Lys-8. An average global SILAC ratio **(A)** of 14.912 indicated complete SILAC labeling of *BY4742.* (**C**) Representative spectra of SRSGVAVADESLTAFNDLK peptide from COF1p, with a calculated SILAC ratio of 15.585. (**D**) Comparison of the growth rates of the *SUB62* and the *BY4742* strains. Growth of *SUB62* (**D'**) and *BY4742* (**D''**) strains on complete media plates (left panels, respectively) and complete media plates lacking lysine (right panels, respectively). **(D')** Growth of *SUB62* on plates lacking lysine was observed after growth in 1l culture, but not when plated from frozen stock. (**D''**) *BY4742* did not grow on plates lacking lysine when plated from either frozen stock or from 1l culture.

**Suppl. Mat. S2: Comparison of Lys-8 labeled *halo$^{AJ}$* with Lys-0 unlabeled *halo$^{AJ}$* embryos. (A)** The distribution of the Lys-8 (H) over Lys-0 (L) protein ratios were found to be centered around 0, when comparing Lys-8 vs. Lys-0 labeled *halo$^{AJ}$* mutants. The upper panel shows H/L ratios of unenriched sample sets (from aliquots drawn before SCX enrichment) and the lower panel H/L ratios after the respective SCX

chromatography. H/L protein ratios represent log2 normalized values. (**B**) Proteins that were found downregulated or upregulated when comparing Lys-8 vs. Lys-0 labeled *halo*$^{AJ}$ mutants. Note that all changes were under the cut-off of 1.1 log2 H/L ratios.

**Suppl. Mat. S3: List of Phosphopeptides**

(**A**) MaxQuant derived evidence file of all phosphopeptides detected in the experiments. (**B**) Extraction of the MaxQuant derived evidence file showing phosphopeptides that were detected in at least 2 biological replicates.

**Table 1: Proteins downregulated in homozygous *htl* mutant embryos**

| proteins | H/L | STDEV |
|---|---|---|
| DNA topoisomerase 2 | -2.15 | 0.76 |
| Clathrin heavy chain | -2.04 | 0.71 |
| Enhancer of mRNA-decapping protein 4 homolog | -1.86 | 0.50 |
| Dynein heavy chain, cytoplasmic | -1.76 | 0.56 |
| SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A,DEAD/H box 1 homolog | -1.73 | 0.55 |
| Myosin heavy chain, non-muscle | -1.73 | 0.50 |
| CG8108 | -1.70 | 0.36 |
| Chromodomain-helicase-DNA-binding protein Mi-2 homolog | -1.62 | 0.42 |
| Nuclear cap-binding protein subunit 1 | -1.49 | 0.47 |
| Polycomb protein l(1)G0020 | -1.46 | 0.35 |
| Coatomer subunit alpha | -1.42 | 0.49 |
| Structural maintenance of chromosomes protein | -1.40 | 0.49 |
| Probable ubiquitin carboxyl-terminal hydrolase FAF | -1.39 | 0.46 |
| Cullin-associated NEDD8-dissociated protein 1 | -1.38 | 0.45 |
| Bifunctional glutamate/proline--tRNA ligase | -1.36 | 0.56 |
| Eukaryotic translation initiation factor 3 subunit A | -1.34 | 0.25 |
| ADP,ATP carrier protein | -1.30 | 0.27 |
| Apollo; Artemis | -1.30 | 0.18 |
| Isoleucyl-tRNA synthetase | -1.27 | 0.45 |
| FACT complex subunit Ssrp1 | -1.25 | 0.27 |
| Mms19 | -1.21 | 0.31 |
| Nucleoporin 50kD | -1.21 | 0.36 |
| Tailor | -1.21 | 0.46 |
| Cullin homolog 1 | -1.20 | 0.37 |
| Tubulin alpha-4 chain | -1.18 | 0.49 |
| Spenito | -1.17 | 0.28 |
| NAT1 | -1.17 | 0.33 |
| mini spindles | -1.16 | 0.40 |
| Probable glutamine--tRNA ligase | -1.16 | 0.19 |
| Eukaryotic translation initiation factor 4G1 | -1.14 | 0.19 |
| Eukaryotic translation initiation factor 3 subunit L | -1.14 | 0.31 |
| Eukaryotic translation initiation factor 3 subunit E | -1.12 | 0.44 |
| Glutathione S-transferase 1-1 | -1.04 | 0.08 |
| Eukaryotic translation initiation factor 3 subunit B | -1.02 | 0.23 |
| Probable 26S proteasome non-ATPase regulatory subunit 3 | -0.99 | 0.24 |
| Apolipophorins;Apolipophorin-2;Apolipophorin-1 | -0.93 | 0.16 |

36 proteins were identified to be downregulated in $htl^{AB42}$ embryos during late stage 7. Normalized H/L ratios are shown for each individual downregulated protein in average calculated from the values of the 3 individual biological replicates. The standard deviation denotes the variation value which was calculated from the individual H/L ratios between the biological replicates.

**Table 2: Proteins upregulated in *htl* homozygous embryos**

| Upregulated proteins | H/L normalised | STDEV |
|---|---|---|
| Asparagine synthetase | 1.61 | 0.05 |
| Dipeptidase B | 1.59 | 0.32 |
| Peptidyl-prolyl cis-trans isomerase | 1.29 | 0.09 |
| Glutathione S-transferase S1 | 1.15 | 0.30 |
| CG6084 | 1.12 | 0.11 |
| Dihydropteridine reductase | 1.00 | 0.15 |
| Succinyl-CoA:3-ketoacid-coenzyme A transferase | 0.94 | 0.15 |
| Probable histone-binding protein Caf1 | 0.91 | 0.29 |
| CTP synthase | 0.78 | 0.25 |
| CG2915 | 0.78 | 0.33 |
| Maltase A5 | 0.78 | 0.21 |
| Nucleoplasmin-like protein | 0.78 | 0.22 |
| Aldehyde dehydrogenase | 0.73 | 0.19 |
| Ecdysone-induced protein 55E | 0.71 | 0.26 |
| Glutathione S transferase E13 | 0.70 | 0.05 |
| Microsomal glutathione S-transferase-like | 0.68 | 0.11 |
| CG4069 | 0.68 | 0.16 |
| CG17337 | 0.67 | 0.26 |
| CG9149 | 0.67 | 0.06 |
| Aldehyde oxidase 1 | 0.67 | 0.23 |
| vibrator | 0.64 | 0.16 |
| alphabet | 0.62 | 0.12 |
| Peptidyl-prolyl cis-trans isomerase | 0.58 | 0.07 |
| CG6028 | 0.58 | 0.10 |
| CG6745 | 0.56 | 0.00 |

25 proteins were identified to be upregulated in *htl*$^{AB42}$ embryos during late stage 7. Normalized H/L ratios are shown for each individual upregulated protein in average calculated from the values of the 3 individual biological replicates. The standard deviation denotes the variation value calculated from the individual H/L ratios between the biological replicates.

**Table 3: Candidates of down- and upregulated proteins according to statistical evidence**

| Downregulated proteins | T-Test Difference |
|---|---|
| eIF2B-epsilon | -4.52 |
| Glutathione S-transferase 1-1 | -3.37 |
| Lethal (2) 41Ab | -2.88 |
| Splicing factor SRp54 | -1.13 |
| ATP-dependent RNA helicase p62 | -1.02 |
| Apolipophorins;Apolipophorin-2;Apolipophorin-1 | -1.02 |
| D-Importin 7/RanBP7 | -0.88 |
| Replication factor C subunit 1 | -0.86 |

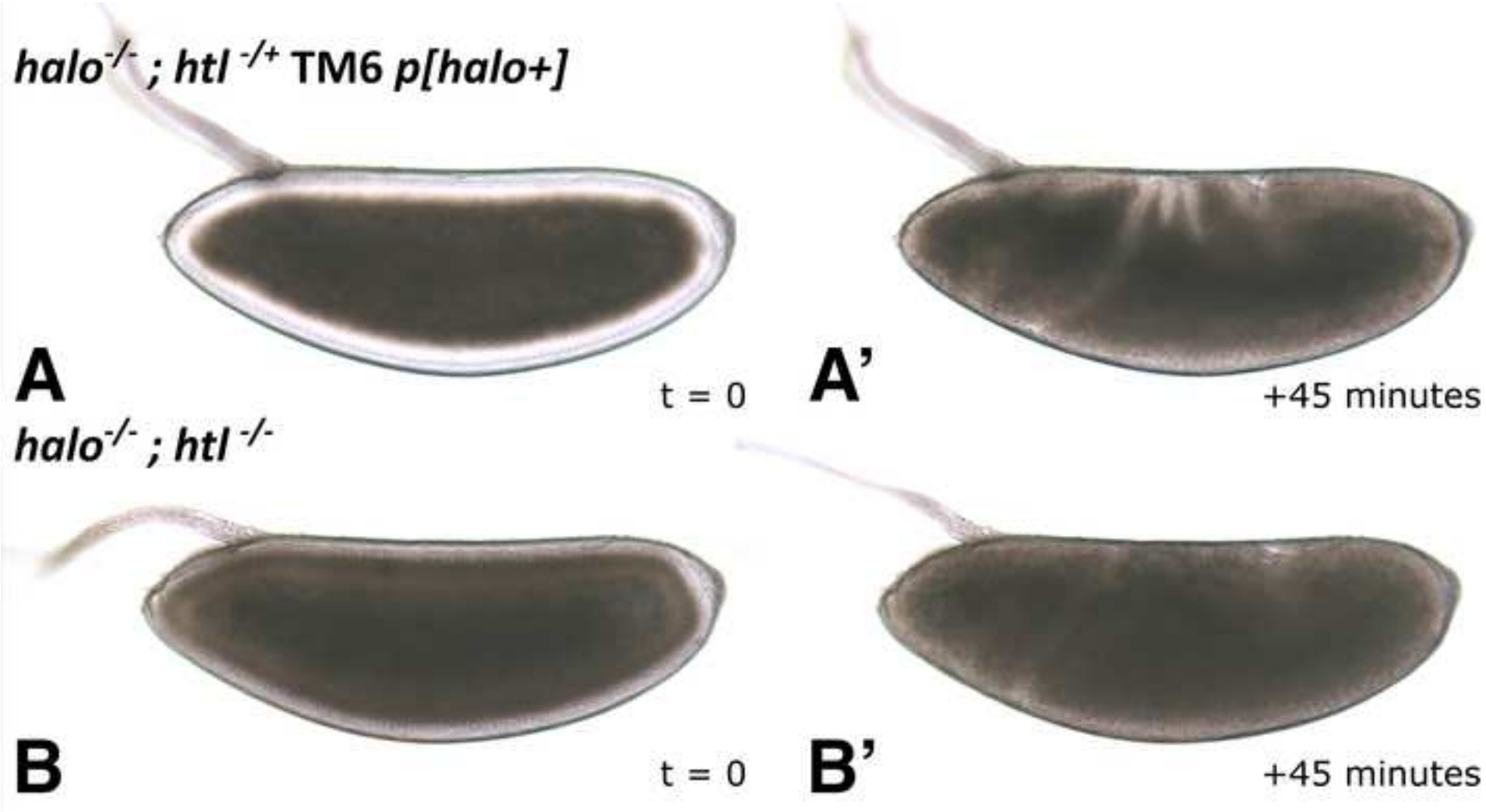
| Upregulated proteins | T-Test Difference |
|---|---|
| Asparagine synthetase | 1.61 |
| Peptidyl-prolyl cis-trans isomerase | 1.36 |
| CG6084 | 1.07 |
| Alpha-mannosidase | 1.05 |
| Dihydropteridine reductase | 0.96 |

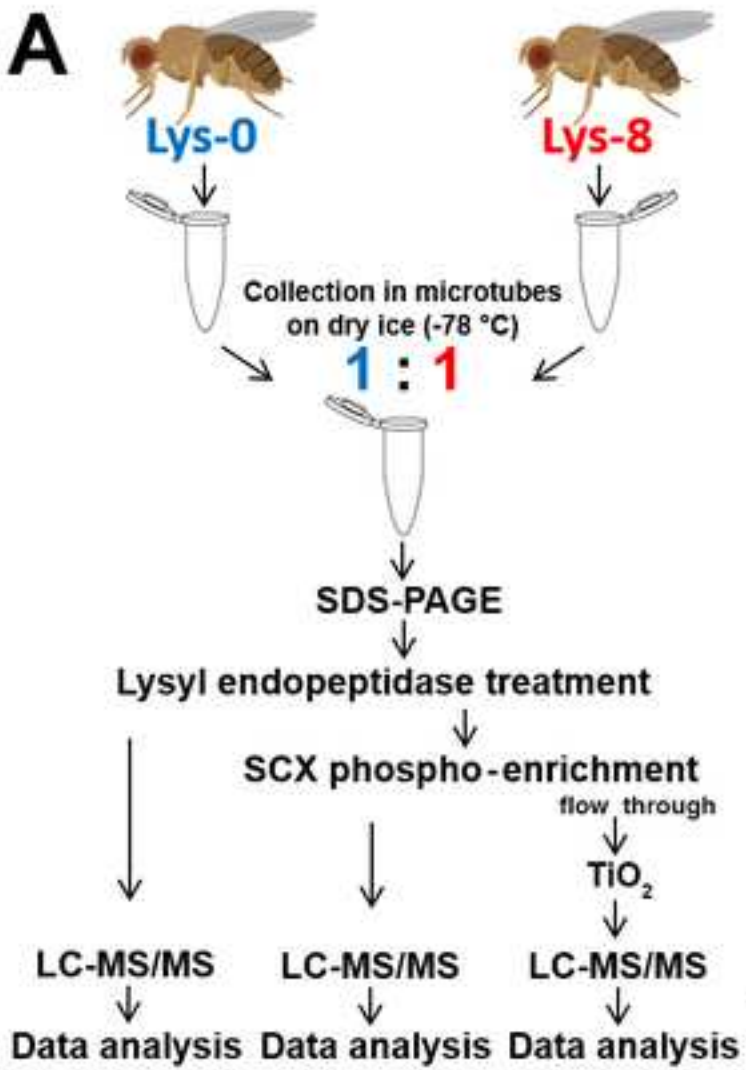
List of protein changes in *htl* mutant embryos, which were revealed by Volcano plot analysis. 5 proteins are found to be upregulated and 8 proteins are downregulated. Averaged normalized H/L ratios between the three biological replicates are shown. The standard deviation denotes the variation between the individual experimental replicates.

**Table 4: Phosphopeptides detected in all 3 bioreplicates**

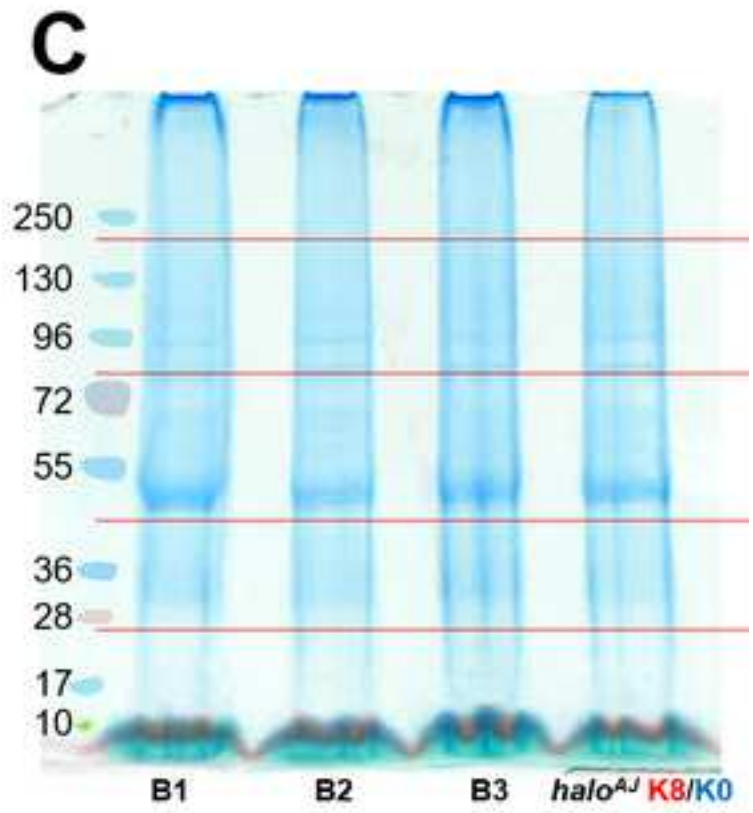
| phosphopeptide | H/L | STDEV | protein,gene | protein H/L | STDEV |
|---|---|---|---|---|---|
| [1]QISIGI**Y*** ELLK | - 5.13 | 1.40 | Garz, CG8487 | -3.50** | 0.09 |
| [1]APATP....PVD**S*** SGSPASPKK | - 2.90 | 0.45 | TppII, CG3991 | 0.06 | 1.04 |
| [1]DVDFGD**S*** DNENEPDAYLARLK | -2.55 | 0.45 | Ssrp1, CG4817 | - 1.25 | 0.27 |
| [1]ASAFQF**S*** DDEEEVK | - 2.06 | 0.87 | eIF3c, CG4954 | - 0.71 | 0.61 |
| [2]ASAFQF**S*** DDEEEVK | - 1.61 | 1.24 | eIF3c, CG4954 | - 0.71 | 0.61 |
| [3]V**T*** ILWMGGSGSIVGKSVLL | - 1.14 | 0.14 | Spoon, CG3249 | - 0.16 | 0.89 |
| [3]A**S*** GVTVSDVCK | - 1.13 | 0.34 | Tsr, CG4254 | - 0.14 | 0.91 |
| [1]NAGGVGVGVGEK**S*** PDLK | - 1.12 | 0.18 | Amun, CG2446 | - 0.28 | 0.82 |
| [1]RKKPEDPSSEAEALC**S*** PAK | - 0.88 | 0.33 | NASP, CG8223 | 0.12 | 1.09 |
| [2]SAEAEAIVTTATADVS**S*** PSK | - 0.80 | 0.21 | NASP, CG8223 | 0.12 | 1.09 |
| [3]SAEAEAIVTTATADVS**S*** PSK | - 0.80 | 0.21 | NASP, CG8223 | 0.12 | 1.09 |
| [1]ALGGIVLTA**S*** HNPGGPENDFGIK | 1.10 | 1.75 | Pgm1, CG5165 | 0.07 | 1.05 |

Phosphopeptides that were detected in all three SCX-enriched samples[1] or in all three $TiO_2$-enriched samples[2] or detected in all three unenriched bioreplicates[3]. The star (*) marks the phosphosite with the highest probability score for each peptide, respectively (see Suppl. File S3). The log2 ratios of the heavy/light populations (H/L) are indicated with their standard deviation (STDEV). The gene names encoding for the respective proteins are indicated with their CG number as annotated in FlyBase (www.Flybase.org). The overall H/L ratios of the respective proteins are indicated with their Standard deviation (STDEV). The full sequence of the phosphopeptide of TppII is APATPQAATSVTNPAAGDGISVQNDPPVD**S***SGSPASPKK. **Note that the sequence coverage of Garz in our data set was very low (1.8%), since only two distinct peptide species were identified for this protein. For all phosphopeptide data see Suppl. Mat. S3A.









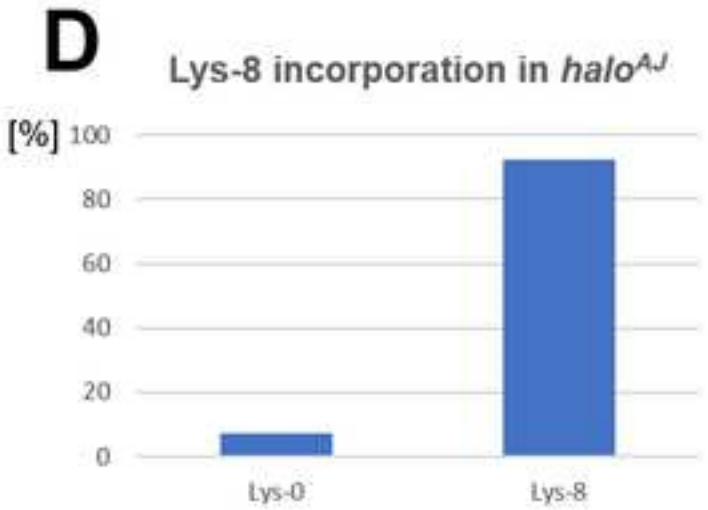
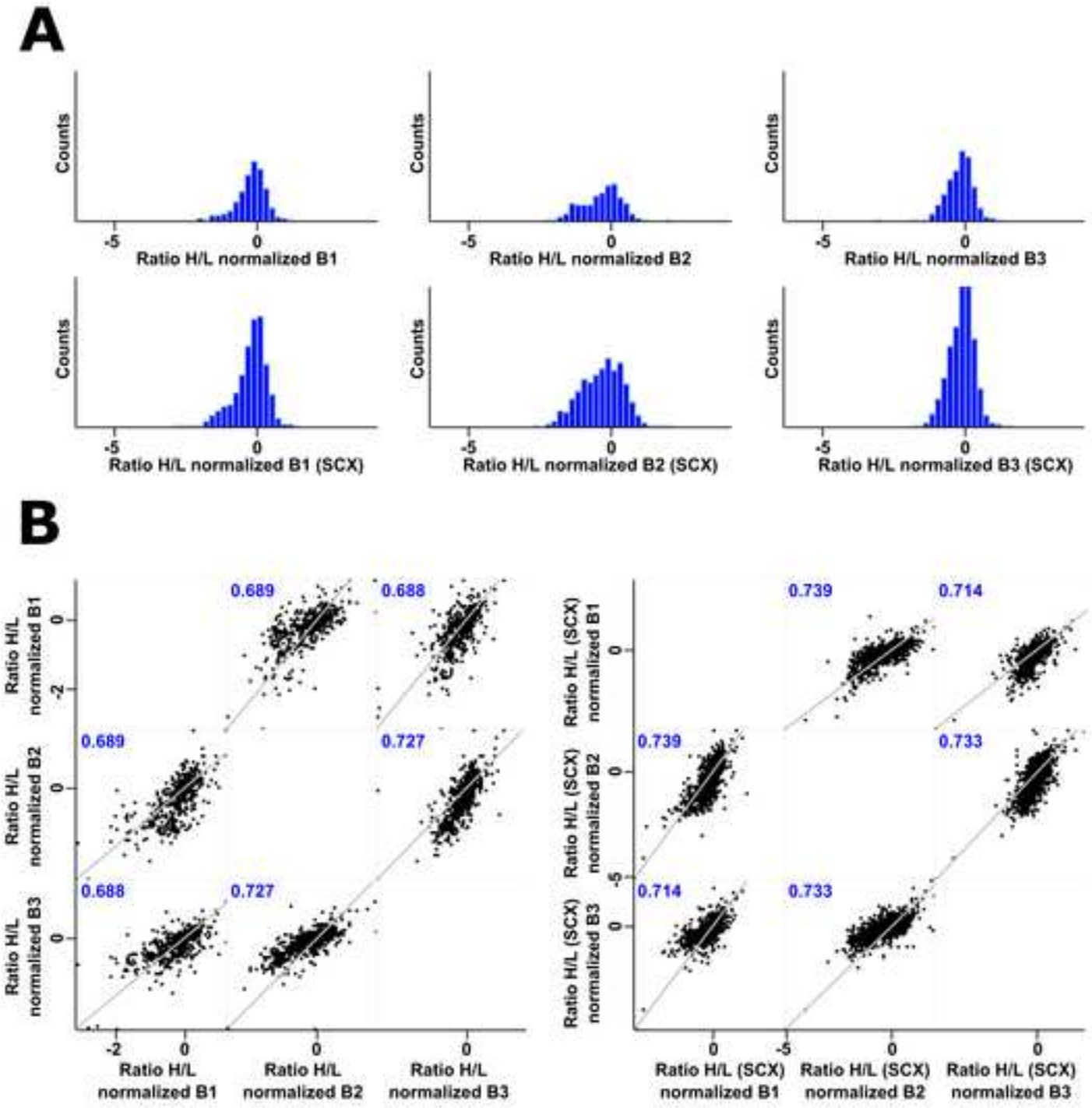



Figure_3

Click here to access/download;Figure;Figure 3.tif



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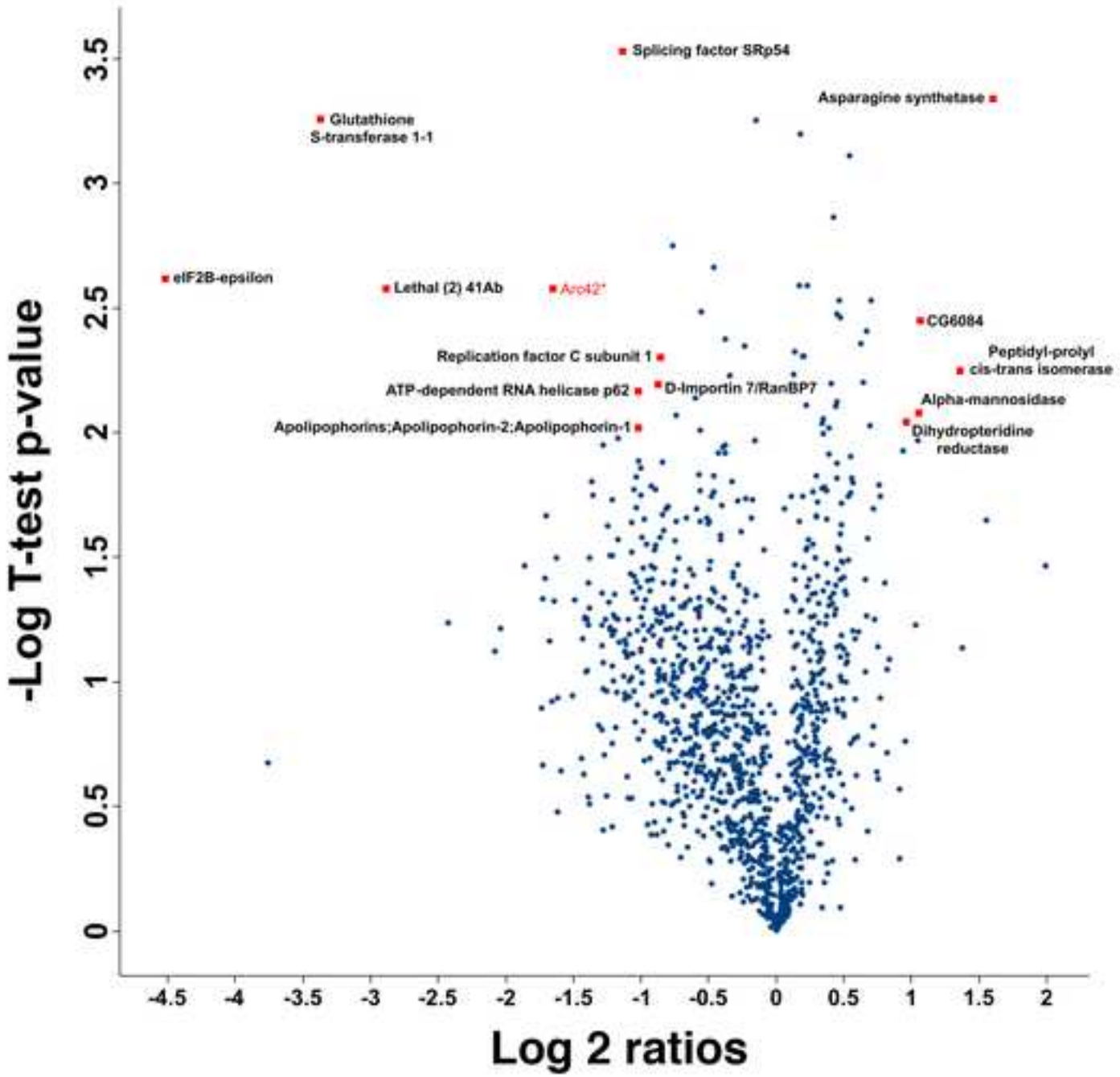

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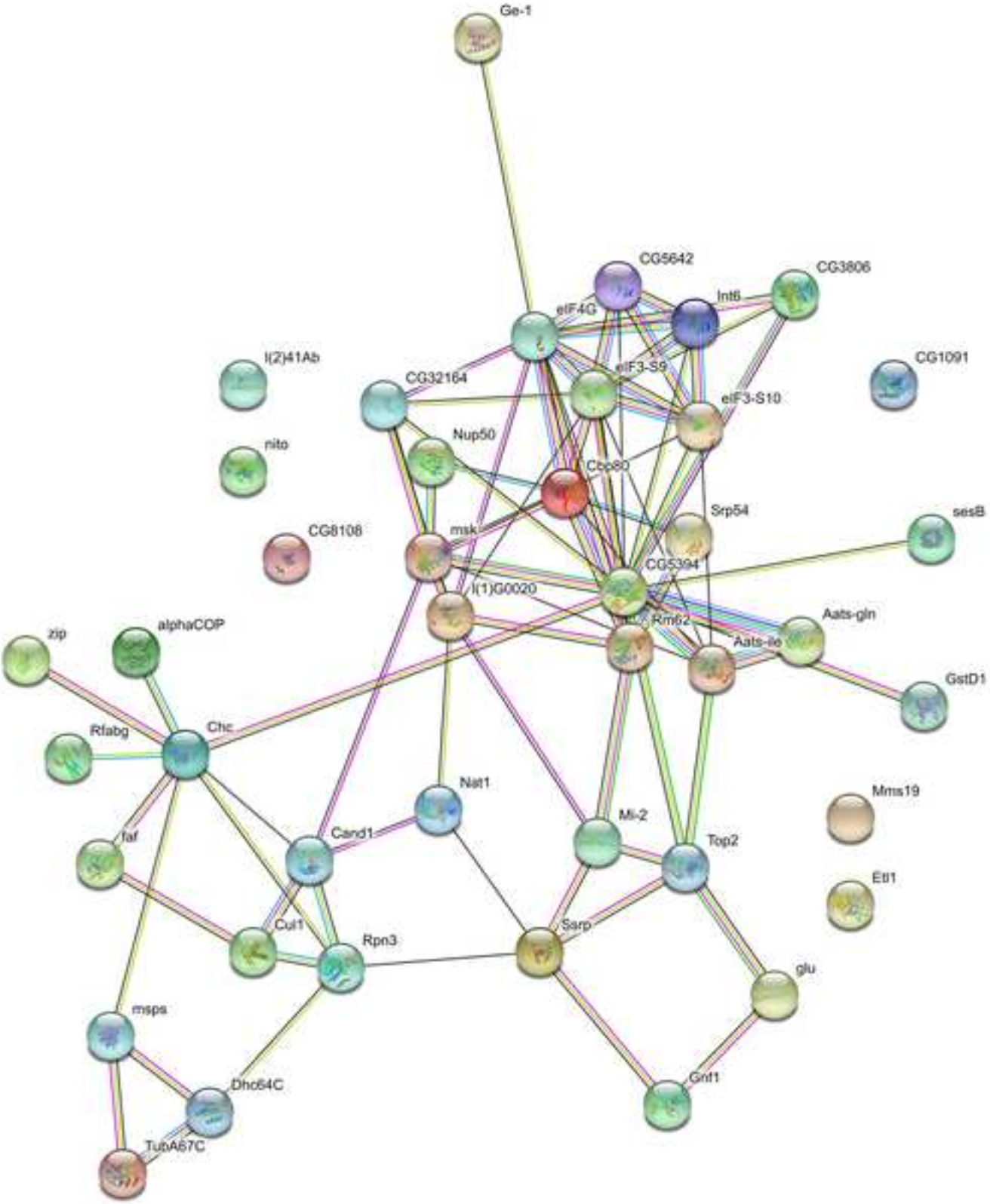

Figure_6

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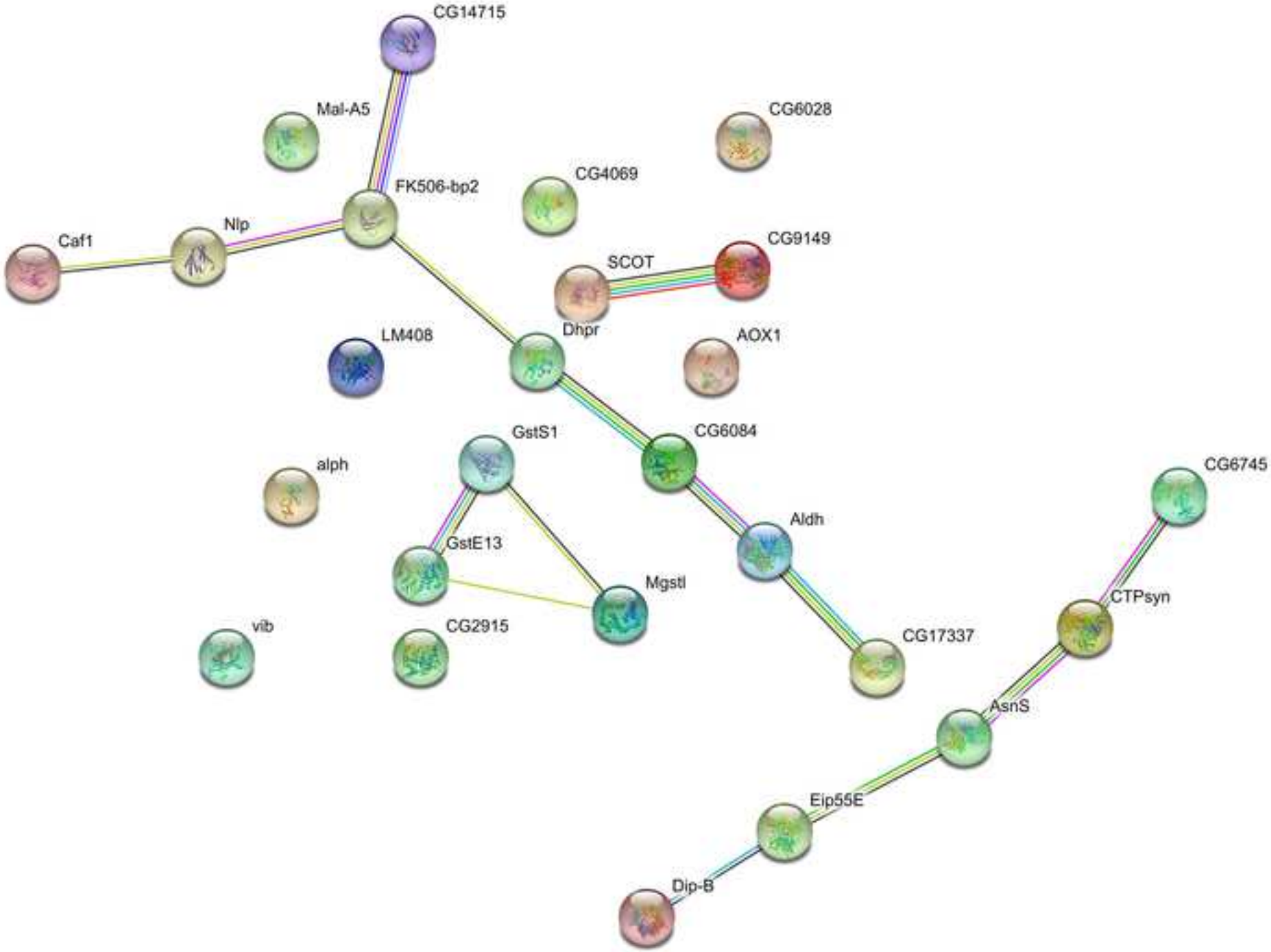
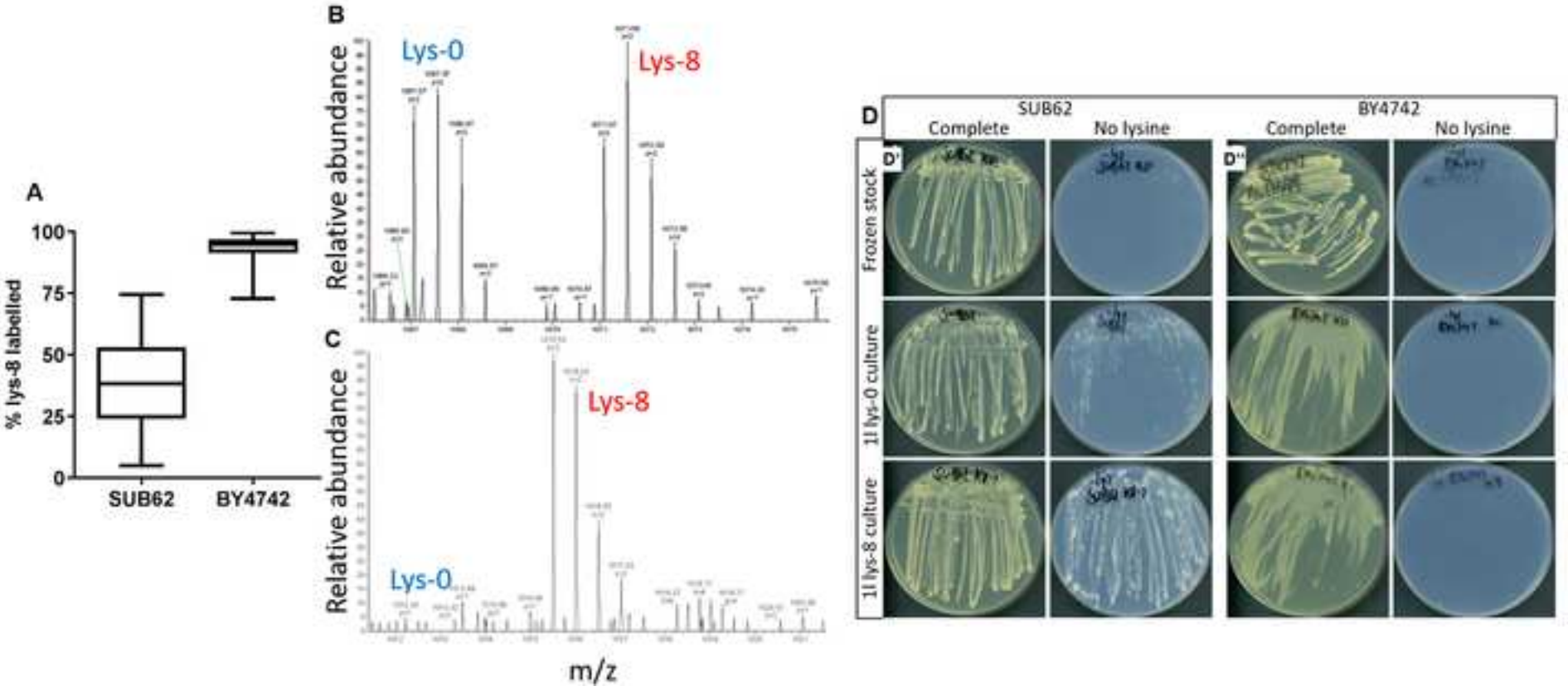
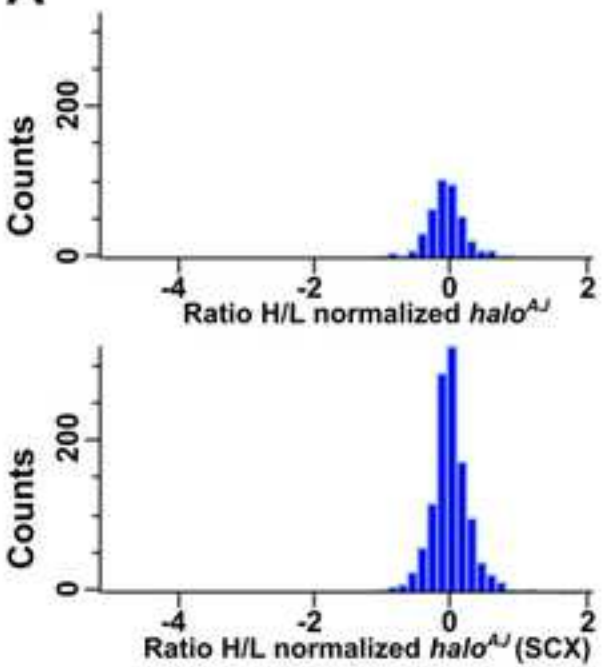




**A**




**B**

| Downregulated proteins *halo*$^{AJ}$/*halo*$^{AJ}$ | H/L normalized |
|---|---|
| Ribosomal protein L27A | -0.489868502 |
| Ribosomal protein S15 | -0.861788418 |
| DNA-polymerase-δ | -0.427498335 |
| Arc42 | -0.460449077 |

| Up-regulated proteins *halo*$^{AJ}$/*halo*$^{AJ}$ | H/L normalized |
|---|---|
| Signal recognition particle receptor β | 0.778965477 |
| Transferrin 1 | 0.356481902 |

| Sequence | Length | K Count | Modifications | Modified seq | Deamidation | Oxidation (M) |
|---|---|---|---|---|---|---|
| AAAPAAVASP | 25 | 1 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 25 | 1 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 25 | 1 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAK_ | | |
| AAAPAAVASP | 25 | 1 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAK_ | | |
| AAAPAAVASP | 26 | 2 | Phospho (STY | _AAAPAAVASPAAAATS(ph)ADASPSPAKK_ | | |
| AAAPAAVASP | 26 | 2 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAKK_ | | |
| AAAPAAVASP | 26 | 2 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 26 | 2 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADAS(ph)PSPA | | |
| AASSAAAQAM | 23 | 1 | Oxidation (M | _AASSAAAQAM(ox)LETS(ph | AASSAAAQAM | |
| ACARGELYSLV | 15 | 1 | Acetyl (Protei | _(ac)ACARGELY(ph)SLVLNTK_ | | |
| ADEKMVTDEI | 10 | 2 | Oxidation (M | _ADEKM(ox)VT(ph)DEK_ | ADEKM(1)VTI | |
| AIELSPGNALF | 14 | 1 | Phospho (STY | _AIELS(ph)PGNALFHAK_ | | |
| AIELSPGNALF | 14 | 1 | Phospho (STY | _AIELS(ph)PGNALFHAK_ | | |
| AKGEILDEVVT | 19 | 3 | 3 Phospho (S | _AKGEILDEVVT(ph)LS(ph)QIS(ph)AKK_ | | |
| ALDLLMSYRLI | 11 | 1 | Oxidation (M | _ALDLLM(ox)S(ph)Y(ph)RLK | ALDLLM(1)SY | |
| ALDLLMSYRLI | 11 | 1 | Oxidation (M | _ALDLLM(ox)S(ph)Y(ph)RLK | ALDLLM(1)SY | |
| ALELSHLKSFV | 12 | 2 | Phospho (STY | _ALELSHLKS(ph)FVK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph | ALGGIVLTASHN(0.529)PGG | |
| ALILNRTGALN | 12 | 1 | Phospho (STY | _ALILN(de)RT | ALILN(1)RTGALN(1)K | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | 2 Phospho (S | _ALQAVYPDYVDELS(ph)LYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | 2 Phospho (S | _ALQAVYPDYVDELS(ph)LYGS(ph)K_ | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APSLHPPHME | 22 | 1 | Oxidation (M | _APS(ph)LHPI | APSLHPPHME | APSLHPPHM( |
| AQDVVGRGA | 17 | 1 | Phospho (STY | _AQDVVGRGAT(ph)NILICNK_ | | |
| AQDVVGRGA | 17 | 1 | Phospho (STY | _AQDVVGRGAT(ph)NILICNK_ | | |
| AQDVVGRGA | 17 | 1 | Phospho (STY | _AQDVVGRGAT(ph)NILICNK_ | | |
| AQNISPEQSG | 18 | 1 | Acetyl (Protei | _(ac)AQNIS(ph)PEQSGGAGGGGSK_ | | |
| ARLVFTEK | 8 | 1 | Acetyl (Protei | _(ac)ARLVFT(ph)EK_ | | |
| ARLVFTEK | 8 | 1 | Acetyl (Protei | _(ac)ARLVFT(ph)EK_ | | |
| ARSLSNSPLYH | 14 | 2 | 3 Phospho (S | _ARS(ph)LS(ph)NS(ph)PLYHRKK_ | | |
| ARSLSNSPLYH | 14 | 2 | 3 Phospho (S | _ARS(ph)LS(ph)NS(ph)PLYHRKK_ | | |
| ARSLSNSPLYH | 14 | 2 | 3 Phospho (S | _ARS(ph)LS(ph)NS(ph)PLYHRKK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)ASGVT(ph)VSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)ASGVT(ph)VSDVCK_ | | |
| ASRHNTASRA | 18 | 1 | 2 Phospho (S | _AS(ph)RHN( | ASRHN(1)TASRAHVITRLVK | |
| CISAVNKQQR | 20 | 2 | 2 Phospho (S | _CIS(ph)AVNI | CISAVNKQ(0.001)Q(0.007)F | |
| CLPDYANKLK | 10 | 2 | Phospho (STY | _CLPDY(ph)ANKLK_ | | |
| CLPDYANKLK | 10 | 2 | Phospho (STY | _CLPDY(ph)ANKLK_ | | |
| DLEYFNNLK | 9 | 1 | Phospho (STY | _DLEY(ph)FN( | DLEYFN(1)N(1)LK | |
| DLEYFNNLK | 9 | 1 | Phospho (STY | _DLEY(ph)FN( | DLEYFN(1)N(1)LK | |
| DMRGTILRRK | 10 | 1 | Oxidation (M | _DM(ox)RGT(ph)ILRRK_ | DM(1)RGTILR | |
| DRQSLFTQVY | 18 | 2 | Phospho (STY | _DRQ(de)SLF | DRQ(0.991)SLFTQ(0.004)VY | |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ | | |
| EAAAGEDITPI | 17 | 1 | Phospho (STY | _EAAAGEDITPLADES(ph)IK_ | | |
| EAAQYGTVNA | 14 | 1 | Phospho (STY | _EAAQY(ph)GTVNAVLPK_ | | |
| EAAQYGTVNA | 14 | 1 | Phospho (STY | _EAAQY(ph)GTVNAVLPK_ | | |
| EANMLQSPV( | 15 | 1 | 2 Oxidation (I | _EANM(ox)LC | EAN(0.004)M | EANM(1)LQSI |
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVSM(ox)AS(ph)PAKD | | EASPVSM(1)A |
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVSM(ox)AS(ph)PAKD | | EASPVSM(1)A |
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVS(ph)M(ox)ASPAKD | | EASPVSM(1)A |
| EFVFQLHGKM | 18 | 3 | Oxidation (M | _EFVFQLHGKM(ox)SNY(ph) | | EFVFQLHGKM |
| EKTDAMAKA( | 16 | 3 | 2 Phospho (S | _EKT(ph)DAMAKAQEFLRT(ph)K_ | | |
| ELGNAEPAPS | 24 | 1 | Phospho (STY | _ELGNAEPAPSVSSTTVSS(ph)PPAGVK_ | | |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | | |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | | |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | | |
| EMIKILQEQAI | 14 | 2 | Phospho (STY | _EMIKILQ(de) | EMIKILQ(0.503)EQ(0.503)A | |
| ENSPSNVAKK | 13 | 3 | 2 Phospho (S | _ENS(ph)PS(p | EN(0.039)SPSN(0.961)VAKK | |
| ENTKNLVTGE | 14 | 2 | Phospho (STY | _EN(de)TKN(( | EN(1)TKN(1)LVTGEPITK | |
| ESAQQLEAQT | 11 | 1 | 2 Phospho (S | _ES(ph)AQ(de | ESAQ(0.854)Q(0.147)LEAQ( | |
| ESTPLSASPKK | 11 | 2 | Phospho (STY | _ESTPLSAS(ph)PKK_ | | |
| ETELMQSKIQ | 20 | 2 | Phospho (STY | _ETELMQSKIQET(ph)LGLDPVDK_ | | |
| ETEQVAQPQF | 20 | 1 | Phospho (STY | _ETEQVAQPC | ETEQ(0.085)VAQ(0.085)PQ( | |
| ETIADIMRVKT | 13 | 2 | 2 Phospho (S | _ET(ph)IADIMRVKT(ph)IK_ | | |
| EVCAQSLQDC | 23 | 2 | Phospho (STY | _EVCAQS(ph) | EVCAQ(0.12)SLQ(0.116)DQ( | |
| EVSDDEADDE | 12 | 2 | Phospho (STY | _EVS(ph)DDEADDEKK_ | | |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( | |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( | |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( | |
| FMSNKNPYSL | 15 | 2 | Oxidation (M | _FMSNKN(de | FMSN(0.008) | FMSNKNPYSL |
| FSSELFKEIIK | 11 | 2 | 2 Phospho (S | _FS(ph)S(ph)ELFKEIIK_ | | |
| GEALTSKQRY( | 13 | 2 | 2 Phospho (S | _GEALT(ph)SI | GEALTSKQ(0.991)RYQ(0.00 | |
| GELQAGKSPF | 11 | 2 | Acetyl (Protei | _(ac)GELQAGKS(ph)PFK_ | | |
| GELQAGKSPF | 11 | 2 | Acetyl (Protei | _(ac)GELQAGKS(ph)PFK_ | | |
| GELQAGKSPF | 11 | 2 | Acetyl (Protei | _(ac)GELQAGKS(ph)PFK_ | | |
| GLGMTKINLI | 12 | 2 | Oxidation (M | _GLGM(ox)T(ph)KINLITK_ | GLGM(1)TKIN | |
| GPQLEDGKVT | 15 | 3 | Oxidation (M | _GPQ(de)LED | GPQ(1)LEDGK | GPQLEDGKVT |
| GQPLVVLSAM | 11 | 1 | Oxidation (M | _GQ(de)PLVV | GQ(1)PLVVLS | GQPLVVLSAM |
| HNNSPNTNLA | 20 | 1 | Phospho (STY | _HN(de)NSPN | HN(0.468)N(0.468)SPN(0.0 | |
| HNNSPNTNLA | 20 | 1 | Phospho (STY | _HN(de)NSPN | HN(0.371)N(0.371)SPN(0.1 | |
| IGEGTYGVVYI | 11 | 1 | Phospho (STY | _IGEGTY(ph)GVVYK_ | | |

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|---|---|---|---|---|---|
| IITHPNFNGNT | 20 | 1 | Phospho (STY | _IITHPN(de)F | IITHPN(0.59)FN(0.205)GN(( |
| IITHPNFNGNT | 20 | 1 | Phospho (STY | _IITHPN(de)F | IITHPN(0.65)FN(0.268)GN(( |
| IKAEHEYRTSM | 20 | 2 | Oxidation (M | _IKAEHEYRTS | IKAEHEYRTSM |
| IKPILQATQTS( | 15 | 1 | Oxidation (M | _IKPILQAT(ph | IKPILQ(0.026) | IKPILQATQTS( |
| IKPILQATQTS( | 15 | 1 | Oxidation (M | _IKPILQAT(ph | IKPILQ(0.005) | IKPILQATQTS( |
| IKPILQATQTS( | 15 | 1 | Oxidation (M | _IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_ | |
| IKPILQATQTS( | 15 | 1 | Oxidation (M | _IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_ | |
| IKPILQATQTS( | 15 | 1 | Oxidation (M | _IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_ | |
| ILFVTESENQA | 21 | 1 | 2 Phospho (S | _ILFVTESEN(c | ILFVTESEN(0.919)Q(0.08)AI |
| ILFVTESENQA | 21 | 1 | 2 Phospho (S | _ILFVTESEN(c | ILFVTESEN(0.919)Q(0.08)AI |
| INQIQMKETN | 14 | 2 | Oxidation (M | _INQIQ(de)M | IN(0.033)Q(0. | INQIQM(1)KE |
| IQVQTKQIAQ | 14 | 2 | Oxidation (M | _IQVQTKQ(de | IQ(0.001)VQ( | IQVQTKQIAQ |
| IQVQTKQIAQ | 14 | 2 | Oxidation (M | _IQVQTKQ(de | IQ(0.011)VQ( | IQVQTKQIAQ |
| IQVQTKQIAQ | 14 | 2 | Phospho (STY | _IQ(de)VQTK( | IQ(0.502)VQ(0.502)TKQ(0.( |
| ISENTIAIISTEL | 17 | 1 | 3 Phospho (S | _IS(ph)ENT(ph)IAIIST(ph)ELEIQK_ | |
| ISMLKQVMSC | 14 | 3 | Oxidation (M | _IS(ph)M(ox)LKQVMS(ph)Q | ISM(0.818)LK |
| KDFLPLAFQM | 19 | 2 | Oxidation (M | _KDFLPLAFQM(ox)QASTGIA | KDFLPLAFQM |
| KDITNLSYKVV | 12 | 3 | Phospho (STY | _KDIT(ph)N(d | KDITN(1)LSYKVVK | |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF | KEESESEDDDI |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF | KEESESEDDDI |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF | KEESESEDDDI |
| KEPTPGEK | 8 | 2 | Phospho (STY | _KEPT(ph)PGEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPESSAKVS(ph)DAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KIEKFQSEEQC | 20 | 3 | Phospho (STY | _KIEKFQS(ph)EEQQQTEDELQDK_ | |
| KIEKFQSEEQC | 20 | 3 | Phospho (STY | _KIEKFQS(ph)EEQQQTEDELQDK_ | |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEESDQS(ph)DDDM(ox) | KKEEESDQSD |
| KKQEESDEEFI | 17 | 3 | Phospho (STY | _KKQEES(ph)DEEFFDLDDIK_ | |
| KLAFSDDESTF | 19 | 2 | Phospho (STY | _KLAFS(ph)DDESTPEEHQGQGK_ | |
| KLIVNGASSNI | 12 | 2 | Phospho (STY | _KLIVN(de)GA | KLIVN(1)GASSN(1)LK | |
| KMEVLSVQNI | 14 | 2 | Phospho (STY | _KMEVLS(ph) | KMEVLSVQ(0.215)N(0.84)H |
| KMKYDFGTLL | 14 | 3 | 2 Phospho (S | _KMKY(ph)DFGT(ph)LLLLVK_ | |
| KNKTNRQLSS | 11 | 3 | Acetyl (Protei | _(ac)KN(de)K | KN(0.97)KTN(0.029)RQ(0.0( |
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |

| | | | | | | |
|---|---|---|---|---|---|---|
| KPEDPSSEAEA | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | | |
| KQEESDEEFFD | 16 | 2 | Phospho (STY | _KQEES(ph)DEEFFDLDDIK_ | | |
| KSAPQSRQSC | 18 | 2 | Phospho (STY | _KS(ph)APQ(( | KSAPQ(1)SRQ(1)SCFRSRPRL | |
| KSKPTAAVTPI | 13 | 3 | 2 Phospho (S | _KS(ph)KPT(p | KSKPTAAVTPIQ(1)K | |
| KVTTIGLNSTA | 14 | 2 | 2 Phospho (S | _KVT(ph)T(ph)IGLNSTAATK_ | | |
| KVTWIGANGI | 15 | 2 | Phospho (STY | _KVT(ph)WIG | KVTWIGAN(0.771)GDQ(0.2 | |
| LDLTIVDLNDE | 19 | 2 | Phospho (STY | _LDLTIVDLNC | LDLTIVDLN(0.079)DEVQ(0.2 | |
| LENLAYEKSED | 24 | 2 | Oxidation (M | _LENLAYEKS(ph)EDLLLT(ph) | LENLAYEKSED | |
| LFEPPVTMRD | 19 | 2 | Phospho (STY | _LFEPPVTMRDMLKSLSRT(ph)K_ | | |
| LGIDIGDRLQA | 15 | 1 | 2 Phospho (S | _LGIDIGDRLQAT(ph)S(ph)RK_ | | |
| LLDFNLLDTDI | 28 | 2 | Phospho (STY | _LLDFNLLDT(ph)DDDDDEEGDEEDKEDTVT | | |
| LNENFVTINIC | 12 | 1 | Phospho (STY | _LN(de)EN(de | LN(0.913)EN(0.913)FVTIN(( | |
| LRFDFNSKAAI | 24 | 3 | 2 Phospho (S | _LRFDFNS(ph | LRFDFN(0.002)SKAAMTIEQ( | |
| LRTSPNEQQK | 16 | 2 | 2 Phospho (S | _LRTS(ph)PN( | LRTSPN(1)EQ(1)Q(1)KDTLHI | |
| LSVQSPPK | 8 | 1 | Phospho (STY | _LSVQS(ph)PPK_ | | |
| LTNGQRQME | 16 | 1 | Oxidation (M | _LT(ph)NGQR | LTN(0.008)GC | LTNGQRQM(1 |
| LTNGQRQME | 16 | 1 | Oxidation (M | _LT(ph)NGQR | LTN(0.016)GC | LTNGQRQM(1 |
| MESTTIVFVTL | 19 | 1 | Oxidation (M | _M(ox)ESTTIV | MESTTIVFVTL | M(1)ESTTIVFV |
| MFLTQQQQLI | 13 | 1 | Oxidation (M | _M(ox)FLT(ph | MFLTQ(0.015 | M(1)FLTQQQ( |
| MFLTQQQQLI | 13 | 1 | Oxidation (M | _M(ox)FLT(ph | MFLTQ(0.138 | M(1)FLTQQQ( |
| MGHLQLDFHS | 13 | 1 | Acetyl (Protei | _(ac)M(ox)GHLQLDFHS(ph) | | M(1)GHLQLD |
| MHKLIMRSVI | 14 | 2 | 2 Oxidation (I | _M(ox)HKLIM(ox)RS(ph)VIN | | M(1)HKLIM(1 |
| MIRATSCALST | 18 | 1 | Oxidation (M | _M(ox)IRATSCALS(ph)TRPLI | | M(1)IRATSCA |
| MLNRCLELVT | 13 | 1 | Oxidation (M | _M(ox)LN(de) | MLN(1)RCLEL | M(1)LNRCLEL |
| MLNRCLELVT | 13 | 1 | Oxidation (M | _M(ox)LN(de)RCLELVT(ph)PFK_ | | |
| MLVRRLLQEL | 18 | 1 | Oxidation (M | _M(ox)LVRRL | MLVRRLLQ(1) | M(1)LVRRLLQ |
| MNDSFGDFN | 23 | 1 | Acetyl (Protei | _(ac)M(ox)NDS(ph)FGDFNA | | M(1)NDSFGD |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | | M(1)PNLQSSI |
| MQHSSMKVD | 15 | 2 | Oxidation (M | _M(ox)Q(de)I | MQ(1)HSSMK | M(0.989)QHS |
| MQIFVKTLTG | 11 | 2 | Acetyl (Protei | _(ac)MQ(de)I | MQ(1)IFVKTLTGK | |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILS( | MQ(0.212)LILSYLQ(0.848)S( | |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY | MQ(0.007)LILSYLQ(0.996)S( | |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_ | | |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_ | | |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)Q(de)I | MQ(0.844)LIL | M(1)QLILSYLC |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)QLILSY | MQ(0.066)LIL | M(1)QLILSYLC |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_ | | |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_ | | |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 | M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 | M(1)RDKISQL |

| | | | | | | |
|---|---|---|---|---|---|---|
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 | M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 | M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 | M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.2 | M(1)RDKISQL |
| MRFISQHNSS | 12 | 1 | Acetyl (Protei | _(ac)M(ox)RF | MRFISQ(0.53 | M(1)RFISQHN |
| MSGALKSQQ( | 13 | 2 | Acetyl (Protei | _(ac)M(ox)SG | MSGALKSQ(0 | M(1)SGALKSC |
| MSLIHSFVTQI | 13 | 1 | 2 Oxidation (I | _M(ox)S(ph)L | MSLIHSFVTQ( | M(1)SLIHSFVT |
| MSQGASEVPI | 16 | 1 | Acetyl (Protei | _(ac)MSQGASEVPLS(ph)ALRLK_ | | |
| MSTIVRK | 7 | 1 | 2 Phospho (S | _MS(ph)T(ph)IVRK_ | | |
| MSTLLENIFAI | 20 | 2 | Oxidation (M | _M(ox)S(ph)T | MSTLLEN(0.9 | M(1)STLLENIF |
| MTEIELPVESV | 26 | 1 | Oxidation (M | _M(ox)TEIELPVESVPSASLS(I | | M(1)TEIELPVE |
| MTIFNLYIFDK | 11 | 1 | Oxidation (M | _M(ox)TIFNLY(ph)IFDK_ | | M(1)TIFNLYIF |
| MVEPSPETVG | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | | M(1)VEPSPET |
| MVEPSPETVG | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | | M(1)VEPSPET |
| MVEPSPETVG | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | | M(1)VEPSPET |
| MYNIYVLKK | 9 | 2 | Phospho (STY | _MYN(de)IY(p | MYN(1)IYVLKK | |
| MYNIYVLKK | 9 | 2 | Phospho (STY | _MY(ph)N(de | MYN(1)IYVLKK | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | | |
| NAGGVGVGV | 18 | 3 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLKK_ | | |
| NAGGVGVGV | 18 | 3 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLKK_ | | |
| NGGILNYMIR | 11 | 1 | Oxidation (M | _N(de)GGILN | N(0.96)GGILN | NGGILNYM(1 |
| NIWKDKTPNL | 11 | 3 | Phospho (STY | _N(de)IWKDK | N(0.999)IWKDKTPN(0.001)I | |
| NKEPLIQIAMT | 20 | 3 | Oxidation (M | _N(de)KEPLIC | N(0.823)KEPL | NKEPLIQIAM( |
| NKLQKNHALI | 23 | 3 | Phospho (STY | _N(de)KLQ(de | N(0.999)KLQ(0.999)KN(0.99 | |
| NLKLQMASTF | 12 | 2 | Oxidation (M | _N(de)LKLQM | N(0.938)LKLC | NLKLQM(1)AS |
| NNIKLKCLIDT( | 20 | 3 | Acetyl (Protei | _(ac)NNIKLKC | N(0.023)N(0.023)IKLKCLIDT | |
| NSQYERESLLK | 11 | 1 | Phospho (STY | _NSQY(ph)ERESLLK_ | | |
| NSQYERESLLK | 11 | 1 | Phospho (STY | _NSQY(ph)ERESLLK_ | | |
| NVGIFIKDDSD | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | | |
| NVGIFIKDDSD | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | | |
| NVGIFIKDDSD | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | | |
| NYPFNIEF | 8 | 0 | Phospho (STY | _N(de)Y(ph)P | N(1)YPFN(1)IEF | |
| PCNLYQTAQE | 13 | 1 | Phospho (STY | _PCNLY(ph)QTAQEQLK_ | | |
| PCNLYQTAQE | 13 | 1 | Phospho (STY | _PCN(de)LY(p | PCN(0.992)LYQ(0.004)TAQ( | |
| PLMQLIIQDTC | 16 | 1 | 2 Oxidation (I | _PLM(ox)QLIIQDTGIGM(ox) | | PLM(1)QLIIQI |
| PLPSGRIPQITI | 17 | 1 | 2 Phospho (S | _PLPS(ph)GRIPQIT(ph)PPASPK_ | | |
| PLPSGRIPQITI | 17 | 1 | 2 Phospho (S | _PLPS(ph)GRIPQIT(ph)PPASPK_ | | |
| PTVAAAAKPA | 34 | 2 | Phospho (STY | _PTVAAAAKPAADDDDDVDLFGS(ph)DDEE | | |
| QELLQSYMK | 9 | 1 | Oxidation (M | _(gl)Q(de)ELL | Q(1)ELLQ(1)S | QELLQSYM(1) |

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|---|---|---|---|---|
| QELLQSYMK | 9 | 1 | Oxidation (M | _(gl)Q(de)ELL Q(1)ELLQ(1)S QELLQSYM(1) |
| QELLQSYMK | 9 | 1 | Phospho (STY | _(gl)Q(de)ELL Q(1)ELLQ(1)SYMK |
| QHSFTSSSALK | 11 | 1 | Phospho (STY | _Q(de)HSFTS Q(1)HSFTSSSALK |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ |
| QISVRGIAEVG | 17 | 1 | Phospho (STY | _(gl)QIS(ph)VRGIAEVGNVTEVK_ |
| QISVRGIAEVG | 17 | 1 | Phospho (STY | _(gl)QIS(ph)VRGIAEVGNVTEVK_ |
| QISVRGIAEVG | 18 | 2 | Phospho (STY | _(gl)QIS(ph)VRGIAEVGNVTEVKK_ |
| QISVRGIAEVG | 18 | 2 | Phospho (STY | _(gl)QIS(ph)VRGIAEVGNVTEVKK_ |
| QIVPLLNYK | 9 | 1 | Phospho (STY | _Q(de)IVPLLN Q(1)IVPLLN(1)YK |
| QKESGEFPEV | 12 | 2 | Phospho (STY | _QKES(ph)GEFPEVGK_ |
| QKFITTEDVNI | 19 | 2 | Oxidation (M | _Q(de)KFIT(p Q(0.941)KFIT QKFITTEDVNI |
| QLRDLETELDE | 14 | 1 | Phospho (STY | _(gl)QLRDLET(ph)ELDEERK_ |
| QLRDLETELDE | 14 | 1 | Phospho (STY | _(gl)QLRDLET(ph)ELDEERK_ |
| QLSIIRQKSLK | 11 | 2 | Phospho (STY | _(gl)Q(de)LSII Q(0.999)LSIIRQ(0.001)KSLK |
| QMPDVETTES | 16 | 1 | Oxidation (M | _Q(de)M(ox)I Q(1)MPDVET QM(1)PDVET |
| QNDLIHDRSLI | 13 | 1 | Phospho (STY | _(gl)QNDLIHDRS(ph)LINK_ |
| QNDLIHDRSLI | 13 | 1 | Phospho (STY | _(gl)QNDLIHDRS(ph)LINK_ |
| QNDLIHDRSLI | 13 | 1 | Phospho (STY | _(gl)QNDLIHDRS(ph)LINK_ |
| QRDLPAPRES | 15 | 1 | Phospho (STY | _(gl)QRDLPAPRES(ph)QSRSK_ |
| QSLIMYFNK | 9 | 1 | Oxidation (M | _Q(de)SLIM(c Q(0.998)SLIM QSLIM(1)YFN |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQA | 18 | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |

| | | | | | |
|---|---|---|---|---|---|
| QSSYHGVHQ/ | 18 | | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | | 1 | Phospho (STY | _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSVPQLANLT | 16 | | 1 | Phospho (STY | _Q(de)SVPQ( |
| QSVPQLANLT | 16 | | 1 | Phospho (STY | _Q(de)SVPQ( |
| QSVPQLANLT | 16 | | 1 | Phospho (STY | _Q(de)SVPQ( |
| QSVPQLANLT | 16 | | 1 | Phospho (STY | _Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_ |
| QSVPQLANLT | 16 | | 1 | Phospho (STY | _Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_ |
| QVEPRQLVRM | 22 | | 1 | Oxidation (M | _QVEPRQLVR |
| QVRTNLQEIQ | 11 | | 1 | Phospho (STY | _(gl)Q(de)VR |
| QVRTNLQEIQ | 11 | | 1 | Phospho (STY | _(gl)Q(de)VRT(ph)NLQEIQ(de)K_ |
| REEENAAAAE | 31 | | 1 | Phospho (STY | _REEENAAAAEEEAGEISATGGATS(ph)PEP |
| REEENAAAAE | 31 | | 1 | Phospho (STY | _REEENAAAAEEEAGEISATGGAT(ph)SPEP |
| REEENAAAAE | 31 | | 1 | Phospho (STY | _REEENAAAAEEEAGEISATGGAT(ph)SPEP |
| RGCQILGLNK | 18 | | 2 | Phospho (STY | _RGCQ(de)IL |
| RGCQILGLNK | 18 | | 2 | Phospho (STY | _RGCQ(de)IL |
| RGCQILGLNK | 18 | | 2 | Phospho (STY | _RGCQ(de)IL |
| RGPPPPPTAS | 17 | | 1 | 2 Phospho (S | _RGPPPPPTA |
| RGPPPPPTAS | 17 | | 1 | 2 Phospho (S | _RGPPPPPTASES(ph)T(ph)RRN(de)K_ |
| RGPPPPPTAS | 17 | | 1 | 2 Phospho (S | _RGPPPPPTASES(ph)T(ph)RRN(de)K_ |
| RIASFKNYISK | 11 | | 2 | Phospho (STY | _RIASFKNY(ph)ISK_ |
| RIQEVYLQK | 9 | | 1 | Phospho (STY | _RIQEVY(ph)L |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RMASSEQPTF | 17 | | 1 | Oxidation (M | _RM(ox)ASSE |
| RPLMLQGHEF | 16 | | 1 | Acetyl (Protei | _(ac)RPLMLQ |
| RPLMLQGHEF | 16 | | 1 | Acetyl (Protei | _(ac)RPLMLQ(de)GHERS(ph)ITQ(de)IK_ |
| SAAVAEGGD/ | 23 | | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGD/ | 23 | | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGD/ | 23 | | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGD/ | 23 | | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGD/ | 23 | | 2 | Phospho (STY | _SAAVAEGGDAVAETAKGEEGS(ph)PK_ |
| SAEAEAIVTTA | 20 | | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |

| | | | | | |
|---|---|---|---|---|---|
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVS(ph)SPSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVS(ph)SPSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ | |
| SASIRILNLINS | 17 | 1 | Oxidation (M | _SASIRILNLIN | SASIRILN(0.0 | SASIRILNLINS |
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVAT(ph)SASPVAAPPATVEK_ | |
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVATS(ph)ASPVAAPPATVEK_ | |
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVAT(ph)SASPVAAPPATVEK_ | |
| SETVDSTEVK | 10 | 1 | Acetyl (Protei | _(ac)S(ph)ET(ph)VDS(ph)T(ph)EVK_ | |
| SHSPPPASNC | 18 | 1 | Acetyl (Protei | _(ac)S(ph)HSPPPASNCEEALIQLK_ | |
| SIQNLNTRDPI | 16 | 1 | Acetyl (Protei | _(ac)S(ph)IQNLNTRDPFADAIK_ | |
| SIQNLNTRDPI | 16 | 1 | Acetyl (Protei | _(ac)S(ph)IQNLNTRDPFADAIK_ | |
| SISEFVDLEAEI | 15 | 1 | Phospho (STY | _S(ph)ISEFVDLEAEDAGK_ | |
| SISEFVDLEAEI | 15 | 1 | Phospho (STY | _S(ph)ISEFVDLEAEDAGK_ | |
| SITMSTISLPAI | 21 | 2 | Oxidation (M | _SIT(ph)MS(ph)TISLPAM(ox | SITM(0.078)S | |
| SITMSTISLPAI | 21 | 2 | 2 Oxidation (I | _SITM(ox)S(ph)T(ph)ISLPAM | SITM(1)STISLI | |
| SITMSTISLPAI | 21 | 2 | 2 Oxidation (I | _SITM(ox)S(ph)T(ph)ISLPAM(ox)LSGVNLK | | |
| SKKSWQARH | 13 | 3 | 2 Phospho (S | _S(ph)KKSWC | SKKSWQ(1)ARHTGIK | |
| SLSRLNTLMK | 10 | 1 | Acetyl (Protei | _(ac)S(ph)LSR | SLSRLN(1)TLM | SLSRLNTLM(1 |
| SLYRISARK | 9 | 1 | Acetyl (Protei | _(ac)S(ph)LYRISARK_ | | |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ | | |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ | | |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ | | |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ | | |

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|---|---|---|---|---|
| SPIVFELTQPS | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPS | 14 | 1 | 2 Phospho (S | _S(ph)PIVFELTQPS(ph)PEK_ |
| SRASFLAQNS | 15 | 1 | 2 Phospho (S | _S(ph)RASFLA SRASFLAQ(0.715)N(0.27)SS |
| SRKHKENLLK | 10 | 3 | Phospho (STY | _S(ph)RKHKE SRKHKEN(1)LLK |
| SSENSEYYSDK | 11 | 1 | Acetyl (Protei | _(ac)S(ph)SENSEYYS(ph)DK_ |
| SSLSVKPNYTL | 12 | 2 | 2 Phospho (S | _S(ph)SLS(ph) SSLSVKPN(1)YTLK |
| STGQLQQLSA | 17 | 1 | Phospho (STY | _STGQLQQLS STGQ(0.007)LQ(0.107)Q(0.1 |
| SVFAEAYDPE | 24 | 1 | Phospho (STY | _S(ph)VFAEAYDPEADDDDDGATAVFPK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| TELAAKLASSL | 26 | 3 | 2 Phospho (S | _TELAAKLAS( TELAAKLASSLVSQ(0.165)GK |
| TIKYLKRVK | 9 | 3 | Phospho (STY | _TIKY(ph)LKRVK_ |
| TKIKIHYIEMTI | 16 | 3 | 2 Phospho (S | _T(ph)KIKIHYIEMT(ph)NVHAK_ |
| TLLNTSPNLLP | 23 | 1 | Phospho (STY | _TLLNTS(ph)PNLLPITTATDTFNNLK_ |
| TLPRNYIHREL | 26 | 1 | 3 Phospho (S | _TLPRNY(ph)IHRELPS(ph)NLT(ph)RAMPST |
| TNISRLGNYFK | 11 | 1 | Acetyl (Protei | _(ac)TNIS(ph)RLGNYFK_ |
| TRRFDEVQMI | 14 | 1 | Oxidation (M | _T(ph)RRFDE TRRFDEVQ(1) TRRFDEVQM( |
| TSKKIIVANSG | 13 | 2 | 2 Phospho (S | _T(ph)SKKIIVANS(ph)GSL_ |
| TSPKPTKPASP | 12 | 3 | Phospho (STY | _TSPKPTKPAS(ph)PK_ |
| TSPKPTKPASP | 12 | 3 | Phospho (STY | _TSPKPTKPAS(ph)PK_ |
| TSWIANPSAV | 26 | 2 | 2 Phospho (S | _T(ph)SWIAN TSWIAN(0.999)PSAVDKLLTI |
| TVNRLSFEKK | 10 | 2 | Phospho (STY | _T(ph)VN(de) TVN(1)RLSFEKK |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEI |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEI |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEI |
| VQEEETVVPQ | 15 | 2 | Phospho (STY | _VQEEETVVPQS(ph)PSKK_ |
| VTDRSHYSPLV | 16 | 1 | Phospho (STY | _VTDRSHYS(ph)PLVSEIAK_ |
| VTDRSHYSPLV | 16 | 1 | Phospho (STY | _VTDRSHYS(ph)PLVSEIAK_ |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIV( VTILWM(1)G( |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIV( VTILWM(1)G( |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIV( VTILWM(1)G( |
| VTKSSSSK | 8 | 2 | Phospho (STY | _VT(ph)KSSSSK_ |
| VTRSTSENIIKM | 16 | 2 | Oxidation (M | _VTRSTSENIIKM(ox)SGT(ph VTRSTSENIIKM |
| VTSKPTLELLSI | 20 | 3 | 2 Phospho (S | _VTSKPTLELLS(ph)PIKPSS(ph)PIK_ |
| VTSKPTLELLSI | 20 | 3 | 2 Phospho (S | _VTSKPTLELLS(ph)PIKPSS(ph)PIK_ |
| VVDTLYQKAK | 10 | 2 | Phospho (STY | _VVDTLY(ph)( VVDTLYQ(1)KAK |
| WEEPFYGGSS | 13 | 1 | Phospho (STY | _WEEPFYGGS(ph)SPAK_ |
| WEEPFYGGSS | 13 | 1 | Phospho (STY | _WEEPFYGGSS(ph)PAK_ |

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|---|---|---|---|---|---|
| YFIESPHPEVL( | 13 | 1 | 2 | Phospho (S | _Y(ph)FIES(ph YFIESPHPEVLQ(1)K |
| YKVPQLEIVPN | 21 | 2 | | Oxidation (M | _YKVPQLEIVPNSAEERLHS(p YKVPQLEIVPN |
| YKVPQLEIVPN | 21 | 2 | | Oxidation (M | _YKVPQLEIVPNSAEERLHS(p YKVPQLEIVPN |
| YLAVGLLDATV | 12 | 1 | | Phospho (STY | _Y(ph)LAVGLLDATVK_ |
| YLAVGLLDATV | 12 | 1 | | Phospho (STY | _Y(ph)LAVGLLDATVK_ |
| YLNQWLHNLI | 10 | 1 | | Phospho (STY | _Y(ph)LNQWI YLN(0.001)Q(0.151)WLHN( |
| YLTVLLSLKTK | 11 | 2 | 2 | Phospho (S | _Y(ph)LTVLLS(ph)LKTK_ |
| YMKLTQEILQI | 11 | 2 | | Phospho (STY | _Y(ph)MKLTC YMKLTQ(1)EILQ(1)K |
| YNLKTPEAP | 9 | 1 | | Phospho (STY | _YN(de)LKT(p YN(1)LKTPEAP |
| YQGQQNDYIL | 17 | 1 | | Phospho (STY | _YQ(de)GQQI YQ(0.25)GQ(0.25)Q(0.25)N( |
| YRLLSANRAA/ | 14 | 1 | | Phospho (STY | _Y(ph)RLLSAN YRLLSAN(1)RAAAVQ(1)K |
| YRQAKMRHIC | 22 | 2 | | Oxidation (M | _YRQ(de)AKM YRQ(1)AKMRI YRQAKMRHIC |

| Phospho (STY | Deamidation | Oxidation (M | Phospho (STY | Acetyl (Protei | Deamidation | Gln->pyro-Glu |
|---|---|---|---|---|---|---|
| AAAPAAVAS(0.997)PAAAAT(0.005)S(0.00 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.995)PAAAAT(0.003)S(0.00 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVASPAAAAT(0.005)S(0.034)ADAS | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVASPAAAAT(0.006)S(0.042)ADAS | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.078)PAAAAT(0.34)S(0.427 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.004)PAAAAT(0.062)S(0.28 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.993)PAAAAT(0.03)S(0.03)A | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.985)PAAAAT(0.077)S(0.08 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAS(0.001)S(0.001)AAAQAI | AASSAAAQAM | | AAS(-27.34)S( | 0 | 0 | 0 |
| ACARGELY(0.814)S(0.183)LVLNT(0.003)K | | | ACARGELY(6.4 | 1 | 0 | 0 |
| ADEKMVT(1)DEK | ADEKM(80.69 | | ADEKMVT(80 | 0 | 0 | 0 |
| AIELS(1)PGNALFHAK | | | AIELS(73.36)F | 0 | 0 | 0 |
| AIELS(1)PGNALFHAK | | | AIELS(80.6)PC | 0 | 0 | 0 |
| AKGEILDEVVT(1)LS(1)QIS(1)AKK | | | AKGEILDEVVT | 0 | 0 | 0 |
| ALDLLMS(1)Y(1)RLK | ALDLLM(45.4 | | ALDLLMS(45.4 | 0 | 0 | 0 |
| ALDLLMS(1)Y(1)RLK | ALDLLM(57.1 | | ALDLLMS(57. | 0 | 0 | 0 |
| ALELS(0.008)HLKS(0.992)FVK | | | ALELS(-21.07) | 0 | 0 | 0 |
| ALGGIVLT(0.066)AS(0.934)HNPGGPENDF | | | ALGGIVLT(-11 | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.784)AS(0.216)HNPGGPENDF | | | ALGGIVLT(5.6 | 0 | 0 | 0 |
| ALGGIVLT(0.121)AS(0.879)HNPGGPENDF | | | ALGGIVLT(-8. | 0 | 0 | 0 |
| ALGGIVLT(0.098)AS(0.902)HNPGGPENDF | | | ALGGIVLT(-9. | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.204)AS(0.796)HNPGGPENDF | | | ALGGIVLT(-5. | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| ALGGIVLT(0.5 | ALGGIVLTASHN(-0.65)PGGF | | ALGGIVLT(0.6 | 0 | 1 | 0 |
| ALILNRT(1)GA | ALILN(44.61)RTGALN(44.61 | | ALILNRT(44.6 | 0 | 2 | 0 |
| ALQAVYPDYVDELS(0.161)LY(0.135)GS(0.7 | | | ALQAVY(-67.3 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.021)LY(0.015)GS(0.9 | | | ALQAVY(-63.3 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.001)LY(0.057)GS(0.9 | | | ALQAVY(-81.2 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.001)LY(0.016)GS(0.9 | | | ALQAVY(-70.6 | 0 | 0 | 0 |
| ALQAVYPDY(0.002)VDELS(0.04)LY(0.004) | | | ALQAVY(-51.2 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.996)LY(0.009)GS(0.9 | | | ALQAVY(-75.9 | 0 | 0 | 0 |
| ALQAVY(0.084)PDY(0.078)VDELS(0.605)L | | | ALQAVY(-10.4 | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.001)VQNL | | | APAT(-56.02) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.001)VQNL | | | APAT(-50.33) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.002)VQNL | | | APAT(-39.76) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.004)VQNL | | | APAT(-40.05) | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| APATPQAATSVTNPAAGDGIS(0.004)VQNI | APAT(-44.28) | 0 | 0 | 0 |
| APS(0.997)LH | APSLHPPHME | APSLHPPHM( | APS(26.22)LH | 0 | 1 | 0 |
| AQDVVGRGAT(1)NILICNK | | | AQDVVGRGA | 0 | 0 | 0 |
| AQDVVGRGAT(1)NILICNK | | | AQDVVGRGA | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| AQNIS(0.997)PEQS(0.003)GGAGGGGSK | | | AQNIS(24.87) | 1 | 0 | 0 |
| ARLVFT(1)EK | | | ARLVFT(64.8 | 1 | 0 | 0 |
| ARLVFT(1)EK | | | ARLVFT(106.2 | 1 | 0 | 0 |
| ARS(0.999)LS(0.999)NS(0.964)PLY(0.038) | | | ARS(32.82)LS | 0 | 0 | 0 |
| ARS(1)LS(0.989)NS(0.852)PLY(0.16)HRKK | | | ARS(33.29)LS | 0 | 0 | 0 |
| ARS(1)LS(1)NS(0.998)PLY(0.003)HRKK | | | ARS(46.06)LS | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-64.04)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-48.64)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-75.24)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-54.82)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-61.47)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-59.12)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-56.8)AFQ | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-42.65)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-66.2)AFQ | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-67.24)AF | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | | | AS(-96.36)AF | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| AS(1)GVTVSDVCK | | | AS(39.82)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | | | AS(38.57)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | | | AS(40.23)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | | | AS(38.02)GVT | 1 | 0 | 0 |
| AS(0.977)GVT(0.022)VSDVCK | | | AS(16.42)GVT | 1 | 0 | 0 |
| AS(0.997)GVT(0.003)VSDVCK | | | AS(25.59)GVT | 1 | 0 | 0 |
| AS(0.42)GVT(0.568)VS(0.012)DVCK | | | AS(-1.31)GVT | 1 | 0 | 0 |
| AS(0.998)GVT(0.002)VSDVCK | | | AS(26.02)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | | | AS(35.02)GVT | 1 | 0 | 0 |
| AS(0.976)GVT(0.023)VS(0.001)DVCK | | | AS(16.37)GVT | 1 | 0 | 0 |
| | | | | 1 | 0 | 0 |
| AS(0.748)RHN | ASRHN(47.22)TASRAHVITRI | | AS(5.52)RHN | 0 | 1 | 0 |
| CIS(1)AVNKQ | CISAVN(-36.09)KQ(-29.43)C | | CIS(58.63)AV | 0 | 1 | 0 |
| CLPDY(1)ANKLK | | | CLPDY(43.63) | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| DLEY(1)FNNL | DLEYFN(65.22)N(65.22)LK | | DLEY(65.22)F | 0 | 2 | 0 |
| DLEY(1)FNNL | DLEYFN(54.07)N(54.07)LK | | DLEY(54.07)F | 0 | 2 | 0 |
| DMRGT(1)ILRRK | | DM(57.55)RG | DMRGT(57.5 | 0 | 0 | 0 |
| DRQSLFT(0.0 | DRQ(24.42)SLFTQ(-24.42)V | | DRQS(-44.49) | 0 | 1 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | | | DVDFGDS(53 | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| DVDFGDS(1)DNENEPDAYLARLK | | DVDFGDS(67. | 0 | 0 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | | DVDFGDS(43. | 0 | 0 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | | DVDFGDS(56. | 0 | 0 | 0 |
| DVDFGDS(0.994)DNENEPDAY(0.006)LARL | | DVDFGDS(22. | 0 | 0 | 0 |
| DVDFGDS(0.999)DNENEPDAY(0.001)LARL | | DVDFGDS(31. | 0 | 0 | 0 |
| EAAAGEDIT(0.001)PLADES(0.999)IK | | EAAAGEDIT(- | 0 | 0 | 0 |
| EAAQY(0.933)GT(0.067)VNAVLPK | | EAAQY(11.44 | 0 | 0 | 0 |
| EAAQY(0.799)GT(0.201)VNAVLPK | | EAAQY(6)GT( | 0 | 0 | 0 |
| EANMLQS(1)I | EAN(-24.31)N | EANM(56.46) | EANMLQS(56 | 0 | 1 | 0 |
| EAS(0.012)PVS(0.157)MAS( | EASPVSM(53. | EAS(-18.36)P | 0 | 0 | 0 |
| EAS(0.014)PVS(0.221)MAS( | EASPVSM(53. | EAS(-17.37)P | 0 | 0 | 0 |
| EAS(0.127)PVS(0.465)MAS( | EASPVSM(40. | EAS(-5.65)PV | 0 | 0 | 0 |
| EFVFQLHGKMS(0.255)NY(0 | EFVFQLHGKM | EFVFQLHGKM | 0 | 0 | 0 |
| EKT(1)DAMAKAQEFLRT(1)K | | EKT(46.68)DA | 0 | 0 | 0 |
| ELGNAEPAPSVSSTTVS(0.286)S(0.713)PPA | | ELGNAEPAPS( | 0 | 0 | 0 |
| ELPDSDSLNVAPPEGFS(1)DEEPEERQCK | | ELPDS(-46.35 | 0 | 0 | 0 |
| ELPDSDSLNVAPPEGFS(1)DEEPEERQCK | | ELPDS(-49.23 | 0 | 0 | 0 |
| ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEP | | ELPDS(-38.75 | 0 | 0 | 0 |
| EMIKILQEQAI | EMIKILQ(0)EQ(0)ALN(19.11 | EMIKILQEQAI | 0 | 2 | 0 |
| ENS(1)PS(1)N | EN(-13.93)SPSN(13.93)VAK | ENS(49.45)PS | 0 | 1 | 0 |
| ENTKNLVT(0.( | EN(40.01)TKN(40.01)LVTGE | ENT(-37.23)K | 0 | 2 | 0 |
| ES(1)AQQLEA | ESAQ(7.67)Q(-7.67)LEAQ(2 | ES(40.73)AQ( | 0 | 2 | 0 |
| ESTPLS(0.351)AS(0.649)PKK | | ES(-36.54)T(- | 0 | 0 | 0 |
| ETELMQS(0.001)KIQET(0.999)LGLDPVDK | | ET(-43.05)ELM | 0 | 0 | 0 |
| ETEQVAQPQF | ETEQ(-11.49)VAQ(-11.49)P( | ET(-42.33)EQ | 0 | 2 | 0 |
| ET(1)IADIMRVKT(1)IK | | ET(47.55)IAD | 0 | 0 | 0 |
| EVCAQS(0.88 | EVCAQ(-12.82)SLQ(-12.82)I | EVCAQS(12.8 | 0 | 2 | 0 |
| EVS(1)DDEADDEKK | | EVS(51.07)DD | 0 | 0 | 0 |
| FFDS(1)GDYQMAK | FFDSGDYQM( | FFDS(40.97)G | 0 | 0 | 0 |
| FFDS(0.994)GDY(0.006)QM | FFDSGDYQM( | FFDS(22.15)G | 0 | 0 | 0 |
| FFDS(1)GDYQMAK | FFDSGDYQM( | FFDS(36.09)G | 0 | 0 | 0 |
| FMSNKNPY(0 | FMSN(-21.26 | FM(-38.75)SN | FMS(-39.87)N | 0 | 1 | 0 |
| FS(1)S(1)ELFKEIIK | | FS(42.43)S(42 | 0 | 0 | 0 |
| GEALT(0.8)S(( | GEALTSKQ(20.61)RYQ(-20.6 | GEALT(5.85)S | 0 | 1 | 0 |
| GELQAGKS(1)PFK | | GELQAGKS(6: | 1 | 0 | 0 |
| GELQAGKS(1)PFK | | GELQAGKS(6( | 1 | 0 | 0 |
| GELQAGKS(1)PFK | | GELQAGKS(6( | 1 | 0 | 0 |
| GLGMT(0.906)KINLIT(0.094 | GLGM(45.65) | GLGMT(9.84) | 0 | 0 | 0 |
| GPQLEDGKVT | GPQ(67.17)LE | GPQLEDGKVT | GPQLEDGKVT | 0 | 1 | 0 |
| GQPLVVLS(1) | GQ(40.62)PL\ | GQPLVVLSAM | GQPLVVLS(4( | 0 | 1 | 0 |
| HNNSPNTNL/ | HN(0)N(0)SPN(-9.76)TN(-15 | HNNS(-46.33) | 0 | 1 | 0 |
| HNNSPNTNL/ | HN(0)N(0)SPN(-4.61)TN(-4.( | HNNS(-52.12) | 0 | 1 | 0 |
| IGEGT(0.186)Y(0.809)GVVY(0.006)K | | IGEGT(-6.39)\ | 0 | 0 | 0 |

| | | | | |
|---|---|---|---|---|
| IIT(0.001)HPN | IITHPN(4.6)FN(-4.6)GN(-4.6 | IIT(-32.2)HPN | 0 | 2 | 0 |
| IITHPNFNGNT | IITHPN(3.85)FN(-3.85)GN(-8 | IIT(-38.2)HPN | 0 | 2 | 0 |
| IKAEHEYRTS(( | IKAEHEYRTSM | IKAEHEYRTSM | IKAEHEY(-42.5 | 0 | 1 | 0 |
| IKPILQAT(0.4! | IKPILQ(-16.83 | IKPILQATQTS( | IKPILQAT(0)Q | 0 | 2 | 0 |
| IKPILQAT(0.3 | IKPILQ(-23.57 | IKPILQATQTS( | IKPILQAT(0)Q | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| ILFVTESENQA | ILFVTESEN(10.6)Q(-10.6)AN | ILFVT(-51.46) | | 0 | 1 | 0 |
| ILFVTESENQA | ILFVTESEN(10.6)Q(-10.6)AN | ILFVT(-51.46) | | 0 | 1 | 0 |
| INQIQMKET(1 | IN(-12.2)Q(-1 | INQIQM(54.2 | INQIQMKET(5 | 0 | 2 | 0 |
| IQVQTKQIAQ | IQ(-30.74)VQ | IQVQTKQIAQ | IQVQT(-61.06 | 0 | 2 | 0 |
| IQVQTKQIAQ | IQ(-21.7)VQ(- | IQVQTKQIAQ | IQVQT(-54.25 | 0 | 2 | 0 |
| IQVQTKQIAQ | IQ(0)VQ(0)TKQ(-12.69)IAQ( | | IQVQT(-41.78 | 0 | 2 | 0 |
| IS(1)ENT(0.999)IAIIS(0.061)T(0.94)ELEIQK | | | IS(34.56)ENT( | 0 | 0 | 0 |
| IS(1)MLKQVMS(1)QLIKK | | ISM(6.54)LKQ | IS(57.43)MLK | 0 | 0 | 0 |
| KDFLPLAFQMQAS(0.227)T( | | KDFLPLAFQM | KDFLPLAFQM | 0 | 0 | 0 |
| KDIT(0.837)N | KDITN(56.04)LSYKVVK | | KDIT(9.69)NL | 0 | 1 | 0 |
| KEES(0.181)ES(0.819)EDDD | | KEESESEDDDI | KEES(-6.55)ES | 0 | 0 | 0 |
| KEES(0.209)ES(0.791)EDDD | | KEESESEDDDI | KEES(-5.78)ES | 0 | 0 | 0 |
| KEES(0.074)ES(0.926)EDDD | | KEESESEDDDI | KEES(-10.98)E | 0 | 0 | 0 |
| KEPT(1)PGEK | | | KEPT(41.43)P | 0 | 0 | 0 |
| KIDNPES(0.333)S(0.333)AKVS(0.333)DAE | | | KIDNPES(0)S( | 0 | 0 | 0 |
| KIDNPES(0.012)S(0.022)AKVS(0.966)DAE | | | KIDNPES(-19. | 0 | 0 | 0 |
| KIDNPES(0.489)S(0.489)AKVS(0.022)DAE | | | KIDNPES(0)S( | 0 | 0 | 0 |
| KIDNPES(0.567)S(0.41)AKVS(0.023)DAEE | | | KIDNPES(1.41 | 0 | 0 | 0 |
| KIEKFQS(1)EEQQQTEDELQDK | | | KIEKFQS(34.8 | 0 | 0 | 0 |
| KIEKFQS(1)EEQQQTEDELQDK | | | KIEKFQS(54.1 | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | | KKEEESDQSD | KKEEES(46.14 | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | | KKEEESDQSD | KKEEES(46.7) | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | | KKEEESDQSD | KKEEES(42.09 | 0 | 0 | 0 |
| KKEEES(0.035)DQS(0.965)D | | KKEEESDQSD | KKEEES(-14.3 | 0 | 0 | 0 |
| KKQEES(1)DEEFFDLDDIK | | | KKQEES(93.2) | 0 | 0 | 0 |
| KLAFS(0.939)DDES(0.054)T(0.007)PEEHQ | | | KLAFS(12.41) | 0 | 0 | 0 |
| KLIVNGAS(0.9 | KLIVN(62.53)GASSN(62.53) | | KLIVNGAS(31 | 0 | 2 | 0 |
| KMEVLS(1)VC | KMEVLSVQ(-6.9)N(6.9)HIQ( | | KMEVLS(44.5 | 0 | 2 | 0 |
| KMKY(1)DFGT(1)LLLLVK | | | KMKY(58.46) | 0 | 0 | 0 |
| KNKT(0.997)N | KN(15.36)KTN(-15.36)RQ(-3 | | KNKT(30.06)N | 1 | 1 | 0 |
| KPEDPSSEAEALCS(1)PAK | | | KPEDPS(-47.0 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | | KPEDPS(-37.5 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | | KPEDPS(-41.9 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | | KPEDPS(-51.7 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | | KPEDPS(-69.7 | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-49.5 | 0 | 0 | 0 |
| KQEES(1)DEEFFDLDDIK | | KQEES(130.5 | 0 | 0 | 0 |
| KS(0.928)APC | KSAPQ(47.92)SRQ(47.92)SC | KS(13.71)APC | 0 | 2 | 0 |
| KS(1)KPT(0.9 | KSKPTAAVTPIQ(46.34)K | KS(43.28)KPT | 0 | 1 | 0 |
| KVT(1)T(0.997) | IGLNS(0.003)TAATK | KVT(37.94)T( | 0 | 0 | 0 |
| KVT(1)WIGAN | KVTWIGAN(5.27)GDQ(-5.27 | KVT(40.09)W | 0 | 1 | 0 |
| LDLT(0.002)I\ | LDLTIVDLN(-9.21)DEVQ(-3.8 | LDLT(-26.77)I | 0 | 1 | 0 |
| LENLAY(0.472) | EKS(0.53)EDI | LENLAYEKSEC | LENLAY(-0.55 | 0 | 0 | 0 |
| LFEPPVT(0.001) | MRDMLKS(0.016)LS(0.20 | LFEPPVT(-31. | 0 | 0 | 0 |
| LGIDIGDRLQAT(1)S(1)RK | | LGIDIGDRLQA | 0 | 0 | 0 |
| LLDFNLLDT(0.999) | DDDDDEEGDEEDKEDT\ | LLDFNLLDT(3 | 0 | 0 | 0 |
| LNENFVT(1)I | LN(9)EN(9)FVTIN(-7.29)IQ( | LNENFVT(41. | 0 | 3 | 0 |
| LRFDFNS(0.9 | LRFDFN(-32.02)SKAAMTIEC | LRFDFNS(20. | 0 | 1 | 0 |
| LRT(0.242)S( | LRTSPN(50.04)EQ(50.04)Q( | LRT(-4.96)S(4 | 0 | 3 | 0 |
| LSVQS(1)PPK | | LS(-82.61)VQ | 0 | 0 | 0 |
| LT(1)NGQRQ | LTN(-22.9)GC | LTNGQRQM(5 | LT(53.12)NGC | 0 | 2 | 0 |
| LT(0.999)NGC | LTN(-20.27)G | LTNGQRQM(4 | LT(40.05)NGC | 0 | 2 | 0 |
| MESTTIVFVTL | MESTTIVFVTL | M(54.95)EST | MES(-53.59)T | 0 | 1 | 0 |
| MFLT(1)QQQ | MFLTQ(-17.6 | M(49.63)FLTC | MFLT(49.63)C | 0 | 2 | 0 |
| MFLT(1)QQQ | MFLTQ(-8.51) | M(68.68)FLTC | MFLT(68.68)C | 0 | 2 | 0 |
| MGHLQLDFHS(1)IPK | | M(44.69)GHL | MGHLQLDFH | 1 | 0 | 0 |
| MHKLIMRS(1)VINNLK | | M(59.98)HKL | MHKLIMRS(5 | 0 | 0 | 0 |
| MIRAT(0.001)S(0.001)CALS | | M(42.82)IRAT | MIRAT(-36.1) | 0 | 0 | 0 |
| MLNRCLELVT | MLN(55.75)R | M(55.75)LNR | MLNRCLELVT | 0 | 1 | 0 |
| | | | | 0 | 1 | 0 |
| MLVRRLLQEL | MLVRRLLQ(4 | M(41.42)LVRI | MLVRRLLQEL | 0 | 2 | 0 |
| MNDS(0.993)FGDFNAT(0.0 | | M(76.82)NDS | MNDS(22.16) | 1 | 0 | 0 |
| MPNLQS(0.857)S(0.121)IPH | | M(56.2)PNLQ | MPNLQS(8.49 | 1 | 0 | 0 |
| MPNLQS(0.492)S(0.492)IPH | | M(40.24)PNL | MPNLQS(0)S( | 1 | 0 | 0 |
| MPNLQS(0.778)S(0.175)IPH | | M(47.71)PNL | MPNLQS(6.47 | 1 | 0 | 0 |
| MPNLQS(0.497)S(0.497)IPH | | M(58.89)PNL | MPNLQS(0)S( | 1 | 0 | 0 |
| MQHS(0.5)S( | MQ(38.01)HS | M(19.78)QHS | MQHS(0)S(0) | 0 | 1 | 0 |
| MQIFVKT(0.5 | MQ(42.8)IFVKTLTGK | | MQIFVKT(0)L | 1 | 1 | 0 |
| MQLILS(0.69 | MQ(-7.66)LILSYLQ(7.66)SQ( | | MQLILS(7.66) | 1 | 3 | 0 |
| MQLILS(0.24 | MQ(-25.8)LILSYLQ(25.8)SQ( | | MQLILS(-4.01 | 1 | 3 | 0 |
| | | | | 1 | 3 | 0 |
| | | | | 1 | 3 | 0 |
| MQLILS(0.97 | MQ(7.74)LILS | M(44.25)QLIL | MQLILS(19.37 | 0 | 2 | 0 |
| MQLILS(0.20 | MQ(-13.61)LI | M(43.69)QLIL | MQLILS(-5.35 | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| MRDKIS(1)QL | MRDKISQ(-15 | M(62.09)RDK | MRDKIS(62.0 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-15 | M(54.34)RDK | MRDKIS(54.3 | 1 | 1 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| MRDKIS(1)QL | MRDKISQ(-10 | M(56.2)RDKIS | MRDKIS(56.2 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-17 | M(51.13)RDK | MRDKIS(51.1 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-12 | M(51.46)RDK | MRDKIS(51.4 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-4.4 | M(43.8)RDKIS | MRDKIS(43.8 | 1 | 1 | 0 |
| MRFIS(0.025) | MRFISQ(0.64 | M(45.21)RFIS | MRFIS(-15.4)( | 1 | 1 | 0 |
| MSGALKS(0.7 | MSGALKSQ(-1 | M(50.15)SGA | MS(-33.15)GA | 1 | 1 | 0 |
| MS(0.417)LIH | MSLIHSFVTQ( | M(54.77)SLIH | MS(0)LIHS(0)I | 0 | 1 | 0 |
| MS(0.002)QGAS(0.01)EVPLS(0.988)ALRLK | | | MS(-26.68)Q( | 1 | 0 | 0 |
| MS(1)T(1)IVRK | | | MS(44.98)T(4 | 0 | 0 | 0 |
| MS(0.5)T(0.5) | MSTLLEN(7.5 | M(43.21)STLL | MS(0)T(0)LLE | 0 | 2 | 0 |
| MTEIELPVESVPS(0.051)AS(( | | M(60.73)TEIE | MT(-56.15)EI | 0 | 0 | 0 |
| MTIFNLY(1)IFDK | | M(46.88)TIFN | MT(-34.52)IFI | 0 | 0 | 0 |
| MVEPSPETVGDFQSVQEEVE | | M(86.56)VEP | MVEPS(-69.6 | 0 | 0 | 0 |
| MVEPSPETVGDFQS(0.245)\ | | M(50.26)VEP | MVEPS(-41.7 | 0 | 0 | 0 |
| MVEPSPETVGDFQS(0.001)\ | | M(50.32)VEP | MVEPS(-37.1 | 0 | 0 | 0 |
| MY(0.401)NI\ | MYN(63.42)IYVLKK | | MY(-1.74)NIY | 0 | 1 | 0 |
| MY(0.636)NI\ | MYN(53.77)IYVLKK | | MY(2.43)NIY( | 0 | 1 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | | NAGGVGVGV | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | | NAGGVGVGV | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | | NAGGVGVGV | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | | NAGGVGVGV | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLKK | | | NAGGVGVGV | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLKK | | | NAGGVGVGV | 0 | 0 | 0 |
| NGGILNY(1)M | N(13.8)GGILN | NGGILNYM(4 | NGGILNY(49.4 | 0 | 1 | 0 |
| NIWKDKT(1)P | N(31.96)IWKDKTPN(-31.96) | | NIWKDKT(52. | 0 | 1 | 0 |
| NKEPLIQIAMT | N(8)KEPLIQ(-8 | NKEPLIQIAM( | NKEPLIQIAMT | 0 | 1 | 0 |
| NKLQKNHALI | N(32.5)KLQ(32.5)KN(32.5)H | | NKLQKNHALI | 0 | 4 | 0 |
| NLKLQMAS(1 | N(12.81)LKLC | NLKLQM(41.6 | NLKLQMAS(4 | 0 | 1 | 0 |
| NNIKLKCLIDT | N(-18.42)N(-18.42)IKLKCLIC | | NNIKLKCLIDT | 1 | 1 | 0 |
| NS(0.002)QY(0.97)ERES(0.029)LLK | | | NS(-27.81)QY | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | | NVGIFIKDDS( | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | | NVGIFIKDDS( | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | | NVGIFIKDDS( | 0 | 0 | 0 |
| NY(1)PFNIEF | N(41.43)YPFN(41.43)IEF | | NY(41.43)PFN | 0 | 2 | 0 |
| PCNLY(0.854)QT(0.146)AQEQLK | | | PCNLY(7.67)C | 0 | 0 | 0 |
| PCNLY(0.962) | PCN(24.93)LYQ(-24.93)TAQ | | PCNLY(14.07) | 0 | 1 | 0 |
| PLMQLIIQDTGIGMT(1)K | | PLM(40.86)Q | PLMQLIIQDT( | 0 | 0 | 0 |
| PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK | | | PLPS(41.55)G | 0 | 0 | 0 |
| PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK | | | PLPS(33.2)GR | 0 | 0 | 0 |
| PTVAAAAKPAADDDDDVDLFGS(1)DDEEDE | | | PT(-35.3)VAA | 0 | 0 | 0 |
| QELLQS(0.87 | Q(51.95)ELLC | QELLQSYM(5 | QELLQS(8.31) | 0 | 2 | 1 |

| | | | | | |
|---|---|---|---|---|---|
| QELLQS(0.84 | Q(41.43)ELLC | QELLQSYM(4 | QELLQS(7.5)Y | 0 | 2 | 1 |
| QELLQS(0.24 | Q(45.02)ELLQ(45.02)SYMK | | QELLQS(-4.96 | 0 | 2 | 1 |
| QHS(0.009)FT | Q(50.79)HSFTSSSALK | | QHS(-16.7)FT | 0 | 1 | 0 |
| QISIGIY(1)ELLK | | | QIS(-47.73)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-48.31)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-46.94)IG | 0 | 0 | 0 |
| QIS(0.001)IGIY(0.999)ELLK | | | QIS(-32.34)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-55.01)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-38.47)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-43.94)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-39.86)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-57.55)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-35.76)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-50.69)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-47.93)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-49.83)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-53)IGIY(5 | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-39.44)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-55.72)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-52.88)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-36.23)IG | 0 | 0 | 0 |
| QIS(1)VRGIAEVGNVTEVK | | | QIS(75.86)VR | 0 | 0 | 1 |
| QIS(1)VRGIAEVGNVTEVK | | | QIS(45.62)VR | 0 | 0 | 1 |
| QIS(1)VRGIAEVGNVTEVKK | | | QIS(87.21)VR | 0 | 0 | 1 |
| | | | | 0 | 0 | 1 |
| QIVPLLNY(1)K | Q(75.74)IVPLLN(75.74)YK | | QIVPLLNY(75. | 0 | 2 | 0 |
| QKES(1)GEFPEVGK | | | QKES(64.64)G | 0 | 0 | 0 |
| QKFIT(0.5)T(0 | Q(12.07)KFIT | QKFITTEDVNI | QKFIT(0)T(0)E | 0 | 1 | 0 |
| QLRDLET(1)ELDEERK | | | QLRDLET(50.9 | 0 | 0 | 1 |
| QLRDLET(1)ELDEERK | | | QLRDLET(46.8 | 0 | 0 | 1 |
| QLSIIRQKS(1) | Q(28.76)LSIIRQ(-28.76)KSLK | | QLS(-42.53)III | 0 | 1 | 1 |
| QMPDVETTES | Q(47.51)MPD | QM(47.51)PD | QMPDVET(-3 | 0 | 1 | 0 |
| QNDLIHDRS(1)LINK | | | QNDLIHDRS(5 | 0 | 0 | 1 |
| QNDLIHDRS(1)LINK | | | QNDLIHDRS(7 | 0 | 0 | 1 |
| QNDLIHDRS(1)LINK | | | QNDLIHDRS(5 | 0 | 0 | 1 |
| QRDLPAPRES(0.569)QS(0.42)RS(0.011)K | | | QRDLPAPRES | 0 | 0 | 1 |
| QS(0.023)LIM | Q(28.35)SLIM | QSLIM(45.37) | QS(-16.46)LIM | 0 | 1 | 0 |
| QSSYHGVHQAWNT(0.042)NQDS(0.957)K | | | QS(-41.5)S(-4 | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.028)NQDS(0.972)K | | | QS(-47.65)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.042)NQDS(0.958)K | | | QS(-80.23)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.001)NQDS(0.999)K | | | QS(-87.48)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.01)NQDS(0.99)K | | | QS(-52.27)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.025)NQDS(0.975)K | | | QS(-60.4)S(-6 | 0 | 0 | 1 |

| | | | | |
|---|---|---|---|---|
| QSSYHGVHQAWNT(0.005)NQDS(0.995)K | QS(-73.94)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.128)NQDS(0.872)K | QS(-48.42)S(- | 0 | 0 | 1 |
| QS(0.014)VP( | Q(21.8)SVPQ(21.8)LAN(20.: | QS(-21.8)VPC | 0 | 3 | 0 |
| QS(0.005)VP( | Q(13.41)SVPQ(14.75)LAN(5 | QS(-25.08)VP | 0 | 3 | 0 |
| QS(0.006)VP( | Q(11.59)SVPQ(18.04)LAN(6 | QS(-24.64)VP | 0 | 3 | 0 |
| | | | 0 | 3 | 0 |
| | | | 0 | 3 | 0 |
| QVEPRQLVRN | Q(-32.88)VEP | QVEPRQLVRN | QVEPRQLVRN | 0 | 1 | 0 |
| QVRT(1)NLQE | Q(0)VRTN(0)LQ(0)EIQ(30.0 | QVRT(64.82)N | 0 | 2 | 1 |
| | | | 0 | 2 | 1 |
| REEENAAAAEEEAGEISAT(0.01)GGAT(0.21 | REEENAAAAE | 0 | 0 | 0 |
| REEENAAAAEEEAGEISAT(0.001)GGAT(0.4 | REEENAAAAE | 0 | 0 | 0 |
| REEENAAAAEEEAGEIS(0.005)AT(0.02)GG/ | REEENAAAAE | 0 | 0 | 0 |
| RGCQILGLNK' | RGCQ(16.13)ILGLN(-16.13)I | RGCQILGLNK' | 0 | 1 | 0 |
| RGCQILGLNK' | RGCQ(7.33)ILGLN(-7.33)KY( | RGCQILGLNK' | 0 | 1 | 0 |
| RGCQILGLNK' | RGCQ(33.24)ILGLN(-33.24)I | RGCQILGLNK' | 0 | 1 | 0 |
| RGPPPPPT(0.( | RGPPPPPTASESTRRN(43.11 | RGPPPPPT(-2 | 0 | 1 | 0 |
| | | | 0 | 1 | 0 |
| | | | 0 | 1 | 0 |
| RIAS(0.064)FKNY(0.898)IS(0.037)K | RIAS(-11.45)F | 0 | 0 | 0 |
| RIQEVY(1)LQI | RIQ(-12.87)EVYLQ(12.87)K | RIQEVY(55.06 | 0 | 1 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-5( | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-3 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4( | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-3 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-5 | 0 | 0 | 0 |
| RMASSEQPT( | RMASSEQ(0)F | RM(67.65)AS | RMAS(-37.42 | 0 | 1 | 0 |
| RPLMLQGHEF | RPLMLQ(40.43)GHERSITQ(4 | RPLMLQGHEF | 1 | 2 | 0 |
| | | | 1 | 2 | 0 |
| SAAVAEGGDAVAET(0.733)AKGEEGS(0.26 | S(-42.23)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.901)AKGEEGS(0.09 | S(-58.47)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.614)AKGEEGS(0.38 | S(-39.38)AAV | 0 | 0 | 0 |
| S(0.001)AAVAEGGDAVAET(0.702)AKGEE( | S(-28.94)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.209)AKGEEGS(0.79 | S(-48.44)AAV | 0 | 0 | 0 |
| SAEAEAIVTTATADVS(0.307)S(0.514)PS(0. | S(-107.65)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.034)S(0.483)PS(0.4 | S(-78.78)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.051)S(0.77)PS(0.1 | S(-102.74)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.007)S(0.496)PS(0.4 | S(-76.49)AEA | 1 | 0 | 0 |
| SAEAEAIVT(0.022)T(0.02)AT(0.067)ADVS( | S(-61.37)AEA | 1 | 0 | 0 |

| | | | | |
|---|---|---|---|---|
| SAEAEAIVTTATADVS(0.01)S(0.495)PS(0.4 | S(-54.67)AEA | 1 | 0 | 0 |
| SAEAEAIVTT(0.001)AT(0.004)ADVS(0.046 | S(-61.79)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.019)S(0.957)PS(0.( | S(-108.85)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.041)S(0.479)PS(0.4 | S(-81.76)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.047)S(0.743)PS(0.. | S(-102.8)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.48)S(0.329)PS(0.1 | S(-50.28)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.045)S(0.421)PS(0.! | S(-119.63)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTAT(0.001)ADVS(0.035)S(0.37 | S(-66.49)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.007)S(0.783)PS(0.. | S(-112.12)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.052)S(0.762)PS(0. | S(-82.71)AEA | 1 | 0 | 0 |
| SAEAEAIVT(0.01)T(0.012)AT(0.04)ADVS(0 | S(-39.1)AEAE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.067)S(0.467)PS(0.4 | S(-77.93)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.021)S(0.489)PS(0.4 | S(-77.91)AEA | 1 | 0 | 0 |
| SAEAEAIVTT(0.002)AT(0.006)ADVS(0.174 | S(-40.69)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.035)S(0.71)PS(0.2! | S(-81.87)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.175)S(0.771)PS(0.( | S(-108.29)AE/ | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.035)S(0.813)PS(0.. | S(-91.77)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.008)S(0.158)PS(0.! | S(-76.74)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.066)S(0.717)PS(0.. | S(-108.3)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.185)S(0.408)PS(0.4 | S(-80.53)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.018)S(0.396)PS(0.! | S(-55.82)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.068)S(0.878)PS(0.( | S(-89.55)AEA | 1 | 0 | 0 |
| | | 1 | 0 | 0 |
| SASIRILNLINS SASIRILN(-15. | SASIRILNLINS | S(-45.57)AS(- | 0 | 1 | 0 |
| S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS( | S(-16.63)DS(- | 1 | 0 | 0 |
| S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0 | S(-18.26)DS(- | 1 | 0 | 0 |
| SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP | S(-34.71)DS(- | 1 | 0 | 0 |
| S(1)ET(1)VDS(1)T(1)EVK | S(47.19)ET(47 | 1 | 0 | 0 |
| S(0.55)HS(0.449)PPPAS(0.001)NCEEALIQL | S(0.88)HS(-0.! | 1 | 0 | 0 |
| S(0.984)IQNLNT(0.016)RDPFADAIK | S(17.92)IQNL | 1 | 0 | 0 |
| S(0.955)IQNLNT(0.045)RDPFADAIK | S(13.27)IQNL | 1 | 0 | 0 |
| S(0.89)IS(0.11)EFVDLEAEDAGK | S(9.1)IS(-9.1)I | 0 | 0 | 0 |
| | | 0 | 0 | 0 |
| S(0.193)IT(0.578)MS(0.578) | SITM(-11.71)S | S(-6.05)IT(0)M | 0 | 0 | 0 |
| S(0.239)IT(0.275)MS(0.533) | SITM(40.18)S | S(-4.82)IT(-4.! | 0 | 0 | 0 |
| SK_ | | | 0 | 0 | 0 |
| S(0.5)KKS(0.5 | SKKSWQ(45.36)ARHTGIK | S(0)KKS(0)WC | 0 | 1 | 0 |
| S(0.5)LS(0.5)F | SLSRLN(52.58 | SLSRLNTLM(5 | S(0)LS(0)RLNT | 1 | 1 | 0 |
| S(0.889)LY(0.111)RISARK | S(9.03)LY(-9.( | 1 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-54.97)PIVF | 0 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-67.16)PIVF | 0 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-63.62)PIVF | 0 | 0 | 0 |
| SPIVFELTQPS(1)PEK | S(-86.11)PIVF | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| SPIVFELTQPS(1)PEK | S(-70.03)PIVF | 0 | 0 | 0 |
| S(1)PIVFELT(0.009)QPS(0.991)PEK | S(40.41)PIVFE | 0 | 0 | 0 |
| S(0.773)RAS(( | SRASFLAQ(4.71)N(-4.71)SS( | S(6.47)RAS(-6 | 0 | 1 | 0 |
| S(1)RKHKENL | SRKHKEN(58.59)LLK | S(58.59)RKHK | 0 | 1 | 0 |
| S(0.397)S(0.397)ENS(0.206)EY(0.038)Y(0. | | S(0)S(0)ENS(- | 1 | 0 | 0 |
| S(0.51)S(0.51 | SSLSVKPN(46.89)YTLK | S(0)S(0)LS(9.2 | 0 | 1 | 0 |
| STGQLQQLS(( | STGQ(-23.59)LQ(-11.38)Q(- | S(-72.86)T(-7 | 0 | 3 | 0 |
| S(0.997)VFAEAY(0.003)DPEADDDDDGAT/ | | S(24.92)VFAE | 0 | 0 | 0 |
| S(0.06)VHS(0.94)PNPGLILQSK | | S(-11.98)VHS( | 1 | 0 | 0 |
| S(0.003)VHS(0.997)PNPGLILQSK | | S(-25.47)VHS( | 1 | 0 | 0 |
| S(0.002)VHS(0.998)PNPGLILQSK | | S(-27.48)VHS( | 1 | 0 | 0 |
| S(0.008)VHS(0.992)PNPGLILQSK | | S(-21.15)VHS( | 1 | 0 | 0 |
| T(0.001)ELAA | TELAAKLASSLVSQ(-4.24)GK | T(-28.81)ELA/ | 0 | 1 | 0 |
| T(0.016)IKY(0.984)LKRVK | | T(-17.9)IKY(1 | 0 | 0 | 0 |
| T(1)KIKIHYIEMT(1)NVHAK | | T(39.99)KIKIH | 0 | 0 | 0 |
| T(0.232)LLNT(0.322)S(0.426)PNLLPIT(0.0 | | T(-2.64)LLNT( | 0 | 0 | 0 |
| T(0.235)LPRNY(0.765)IHRELPS(0.839)NLT | | T(-5.33)LPRN | 0 | 0 | 0 |
| T(0.032)NIS(0.963)RLGNY(0.005)FK | | T(-14.81)NIS( | 1 | 0 | 0 |
| T(1)RRFDEVQ | TRRFDEVQ(6 | TRRFDEVQM( | T(56.33)RRFD | 0 | 2 | 0 |
| T(0.971)S(0.03)KKIIVANS(0.992)GS(0.006 | | T(15.33)S(-15 | 0 | 0 | 0 |
| TSPKPT(0.028)KPAS(0.972)PK | | T(-33.19)S(-3 | 0 | 0 | 0 |
| TSPKPT(0.079)KPAS(0.921)PK | | T(-51.25)S(-4 | 0 | 0 | 0 |
| T(0.432)S(0.4 | TSWIAN(33.19)PSAVDKLLTI | T(0)S(0)WIAN | 0 | 1 | 0 |
| T(0.98)VNRLS | TVN(61.16)RLSFEKK | T(16.84)VNRL | 0 | 1 | 0 |
| VDRS(0.006)DNAAES(0.994)FDDAVEERVI | | VDRS(-22.51) | 1 | 0 | 0 |
| VDRS(0.003)DNAAES(0.997)FDDAVEERVI | | VDRS(-24.86) | 1 | 0 | 0 |
| VDRS(0.007)DNAAES(0.993)FDDAVEERVI | | VDRS(-21.63) | 1 | 0 | 0 |
| VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA | | VNS(-28.14)L | 0 | 0 | 0 |
| VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA | | VNS(-29.34)L | 0 | 0 | 0 |
| VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA | | VNS(-31.63)L | 0 | 0 | 0 |
| VQEEET(0.008)VVPQS(0.566)PS(0.426)KK | | VQEEET(-18.4 | 0 | 0 | 0 |
| VTDRS(0.002)HY(0.002)S(0.996)PLVSEIAK | | VT(-36.61)DR | 0 | 0 | 0 |
| VT(0.001)DRS(0.001)HY(0.016)S(0.983)PL | | VT(-31.81)DR | 0 | 0 | 0 |
| VT(0.996)ILWMGGS(0.003) | VTILWM(47.5 | VT(24.72)ILW | 0 | 0 | 0 |
| VT(0.996)ILWMGGS(0.002) | VTILWM(42.3 | VT(27.11)ILW | 0 | 0 | 0 |
| VT(0.999)ILWMGGS(0.001) | VTILWM(42.0 | VT(32.61)ILW | 0 | 0 | 0 |
| VT(0.999)KSSSSK | | VT(37.92)KS(- | 0 | 0 | 0 |
| VTRS(0.001)T(0.001)S(0.00 | VTRSTSENIIKI | VT(-38.2)RS(- | 0 | 0 | 0 |
| VT(0.007)S(0.018)KPT(0.035)LELLS(0.946) | | VT(-22.82)S(- | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| VVDT(0.012)L | VVDTLYQ(61.76)KAK | VVDT(-19.29) | 0 | 1 | 0 |
| WEEPFY(0.002)GGS(0.885)S(0.114)PAK | | WEEPFY(-27.5 | 0 | 0 | 0 |
| WEEPFY(0.001)GGS(0.472)S(0.528)PAK | | WEEPFY(-28.4 | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| Y(1)FIES(1)PH | YFIESPHPEVLQ(45.08)K | Y(45.08)FIES( | 0 | 1 | 0 |
| YKVPQLEIVPNS(0.166)AEER | YKVPQLEIVPN | Y(-53.17)KVP( | 0 | 0 | 0 |
| YKVPQLEIVPNS(0.211)AEER | YKVPQLEIVPN | Y(-51.88)KVP( | 0 | 0 | 0 |
| Y(1)LAVGLLDATVK | | Y(60.29)LAVG | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| Y(1)LNQWLHI | YLN(-30.03)Q(-7.5)WLHN(7 | Y(56.92)LNQ\ | 0 | 1 | 0 |
| Y(0.999)LT(0.001)VLLS(0.5)LKT(0.5)K | | Y(27.41)LT(-2 | 0 | 0 | 0 |
| Y(1)MKLTQEI | YMKLTQ(70.94)EILQ(70.94) | Y(40.77)MKL | 0 | 2 | 0 |
| Y(0.32)NLKT(( | YN(57.05)LKTPEAP | Y(-3.27)NLKT( | 0 | 1 | 0 |
| YQGQQNDYIL | YQ(0)GQ(0)Q(0)N(0)DYILISL | Y(-62.08)QGC | 0 | 1 | 0 |
| Y(0.999)RLLS( | YRLLSAN(53.38)RAAAVQ(5 | Y(32.42)RLLS( | 0 | 2 | 0 |
| YRQAKMRHIC | YRQ(47.73)AI | YRQAKM(-46. | Y(-34.93)RQA | 0 | 1 | 0 |

| Oxidation (M | Phospho (STY | Missed cleava | Proteins | Leading Prote | Leading Razo | Gene Names |
|---|---|---|---|---|---|---|
| 0 | 2 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 1 | 1 | 0 | A0APA5;Q8M | A0APA5 | A0APA5 | CG3509;BigH1 |
| 0 | 1 | 0 | Q9VK33-2 | Q9VK33-2 | Q9VK33-2 | Sfmbt |
| 1 | 1 | 1 | A0A0B4KHE9 | A0A0B4KHE9 | A0A0B4KHE9 | Rpn2 |
| 0 | 1 | 0 | E2QD63;Q86I | E2QD63 | E2QD63 | HIP-R;HIP |
| 0 | 1 | 0 | E2QD63;Q86I | E2QD63 | E2QD63 | HIP-R;HIP |
| 0 | 3 | 2 | A0A0B4LFB8; | A0A0B4LFB8 | A0A0B4LFB8 | Opa1;opa1-lik |
| 1 | 2 | 0 | Q4V3Q5;Q8M | Q4V3Q5 | Q4V3Q5 | Obp22a CG3 |
| 1 | 2 | 0 | Q4V3Q5;Q8M | Q4V3Q5 | Q4V3Q5 | Obp22a |
| 0 | 1 | 1 | Q8T9C5;Q9I7 | Q8T9C5 | Q8T9C5 | MRP CG6214 |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | M9PB68;Q9V | M9PB68 | M9PB68 | poe |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 2 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 2 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 1 | A0A0B4LGC0; | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 1 | 1 | 0 | A4V201;E1JI1 | A4V201 | A4V201 | Taf4 |
| 0 | 1 | 0 | | REV__Q8I725 | REV__Q8I725 | |
| 0 | 1 | 0 | | REV__Q8I725 | REV__Q8I725 | |
| 0 | 1 | 0 | | REV__Q8I725 | REV__Q8I725 | |
| 0 | 1 | 0 | Q9VTY6 | Q9VTY6 | Q9VTY6 | vih |
| 0 | 1 | 0 | Q8T3J9 | Q8T3J9 | Q8T3J9 | |
| 0 | 1 | 0 | Q8T3J9 | Q8T3J9 | Q8T3J9 | |
| 0 | 3 | 1 | Q8I0A1 | Q8I0A1 | Q8I0A1 | SNF4Agamma |
| 0 | 3 | 1 | Q8I0A1 | Q8I0A1 | Q8I0A1 | SNF4Agamma |
| 0 | 3 | 1 | Q8I0A1 | Q8I0A1 | Q8I0A1 | SNF4Agamma |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2; | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 2 | 0 | Q8IH82 | Q8IH82 | Q8IH82 | grsm |
| 0 | 2 | 2 | A4V449;Q6NI | A4V449 | A4V449 | ND75 |
| 0 | 1 | 1 | F3YDM3;Q6A | F3YDM3 | F3YDM3 | CG32068-RB; |
| 0 | 1 | 1 | F3YDM3;Q6A | F3YDM3 | F3YDM3 | CG32068-RB; |
| 0 | 1 | 0 | Q9V5R2;A1Z8 | Q9V5R2 | Q9V5R2 | Pex6 |
| 0 | 1 | 0 | Q9V5R2;A1Z8 | Q9V5R2 | Q9V5R2 | Pex6 |
| 1 | 1 | 0 | M9PBZ3;M9P | M9PBZ3 | M9PBZ3 | spen |
| 0 | 1 | 1 | Q9VBX4 | Q9VBX4 | Q9VBX4 | CG31510-RA |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |

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|---|---|---|---|---|---|---|---|
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| | | | | | | | |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp | |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp | |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp | |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp | |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp | |
| 0 | 1 | 0 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 | |
| 0 | 1 | 0 | Q9VAN0 | Q9VAN0 | Q9VAN0 | CG11899 | |
| 0 | 1 | 0 | Q9VAN0 | Q9VAN0 | Q9VAN0 | CG11899 | |
| 2 | 1 | 0 | D7FAM9;D7F | D7FAM9 | D7FAM9 | gr97a;Gr97a- | |
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;A | |
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;A | |
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;A | |
| 1 | 1 | 2 | Q7KTG2 | Q7KTG2 | Q7KTG2 | Apoltp | |
| 0 | 2 | 2 | A0A0C4DHG6 | A0A0C4DHG6 | A0A0C4DHG6 | Gel | |
| 0 | 1 | 0 | Q8SYN6;Q9V: | Q8SYN6 | Q8SYN6 | CG8209 | |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | | |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | | |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | | |
| 0 | 1 | 1 | Q9VP27;M9P | Q9VP27 | Q9VP27 | Glg1 | |
| 0 | 2 | 2 | O61380;A8D2 | O61380 | O61380 | eIF4G | |
| 0 | 1 | 1 | Q9VHR8-2;Q9 | Q9VHR8-2 | Q9VHR8-2 | DppIII;CG561 | |
| 0 | 2 | 0 | M9NGE4;M9I | M9NGE4 | M9NGE4 | mud | |
| 0 | 1 | 1 | Q8T410;Q0KH | Q8T410 | Q8T410 | Cnx99A;Cnx1 | |
| 0 | 1 | 1 | Q9V9Z1 | Q9V9Z1 | Q9V9Z1 | mRpL32 | |
| 0 | 1 | 0 | Q9XZ34;Q4V9 | Q9XZ34 | Q9XZ34 | Rif1;CG30085 | |
| 0 | 2 | 1 | P91875 | P91875 | P91875 | RpI1 | |
| 0 | 1 | 1 | Q0PQ31;Q0P | Q0PQ31 | Q0PQ31 | Klp61F | |
| 0 | 1 | 1 | M9PBL3;P028 | M9PBL3 | M9PBL3 | Hsp83 | |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos | |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos | |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos | |
| 1 | 1 | 1 | Q8IA36;Q9W | Q8IA36 | Q8IA36 | mRpS29 | |
| 0 | 2 | 1 | Q6V6U1;Q6V | Q6V6U1 | Q6V6U1 | nec | |
| 0 | 2 | 1 | Q9U6X3;Q9V | Q9U6X3 | Q9U6X3 | MTA1-like | |
| 0 | 1 | 1 | Q9VRQ4 | Q9VRQ4 | Q9VRQ4 | | |
| 0 | 1 | 1 | Q9VRQ4 | Q9VRQ4 | Q9VRQ4 | | |
| 0 | 1 | 1 | Q9VRQ4 | Q9VRQ4 | Q9VRQ4 | | |
| 1 | 1 | 1 | Q9VSM8;Q95 | Q9VSM8 | Q9VSM8 | GAPsec | |
| 1 | 1 | 2 | Q9VH81 | Q9VH81 | Q9VH81 | PpD3 | |
| 1 | 1 | 0 | Q0E9E2;Q86N | Q0E9E2;Q7KN | Q7KN97 | BcDNA:GH06 | |
| 0 | 1 | 0 | B4F4Z1;Q9W4 | B4F4Z1 | B4F4Z1 | CG12681 | |
| 0 | 1 | 0 | B4F4Z1;Q9W4 | B4F4Z1 | B4F4Z1 | CG12681 | |
| 0 | 1 | 0 | C0MJ66;P235 | C0MJ66 | C0MJ66 | CG5363;cdc2 | |
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|---|---|---|---|---|---|---|---|
| 0 | 1 | 0 | CON__P0076 | CON__P0076 | CON__P00761 | | |
| 0 | 1 | 0 | CON__P0076 | CON__P0076 | CON__P00761 | | |
| 1 | 2 | 1 | Q9VVI1 | Q9VVI1 | Q9VVI1 | | |
| 1 | 1 | 1 | | REV__Q95S3 | REV__Q95S34 | | |
| 1 | 1 | 1 | | REV__Q95S3 | REV__Q95S34 | | |
| 1 | 1 | 1 | | REV__Q95S3 | REV__Q95S34 | | |
| 1 | 1 | 1 | | REV__Q95S3 | REV__Q95S34 | | |
| 1 | 1 | 1 | | REV__Q95S3 | REV__Q95S34 | | |
| 0 | 2 | 0 | | REV__Q9VPU | REV__Q9VPU | CG13950 | |
| 0 | 2 | 0 | | REV__Q9VPU | REV__Q9VPU | CG13950 | |
| 1 | 1 | 1 | Q961E0;Q5BI | Q961E0 | Q961E0 | Cul4 | |
| 1 | 1 | 1 | M9PBI9;M9P | M9PBI9 | M9PBI9 | sls | |
| 1 | 1 | 1 | M9PBI9;M9P | M9PBI9 | M9PBI9 | sls | |
| 0 | 1 | 1 | M9PBI9;M9P | M9PBI9 | M9PBI9 | sls | |
| 0 | 3 | 0 | P35875;P358 | P35875 | P35875 | Parp | |
| 1 | 2 | 2 | A8JV07;B4F5I | A8JV07 | A8JV07 | CG9915;CG9 | |
| 1 | 1 | 1 | Q867Z4-3 | Q867Z4-3 | Q867Z4-3 | lola | |
| 0 | 1 | 2 | A0A0B4LFD2; | A0A0B4LFD2 | A0A0B4LFD2 | Hsc70-5 | |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;Rpl | |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;Rpl | |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;Rpl | |
| 0 | 1 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep | |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 | |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 | |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 | |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 | |
| 0 | 1 | 2 | CON__P0266 | CON__P0266 | CON__P02666 | | |
| 0 | 1 | 2 | CON__P0266 | CON__P0266 | CON__P02666 | | |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 | |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 | |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 | |
| 1 | 1 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 | |
| 0 | 1 | 2 | Q9VCC0 | Q9VCC0 | Q9VCC0 | CHORD | |
| 0 | 1 | 1 | M9PE74;Q9W | M9PE74 | M9PE74 | nocte | |
| 0 | 1 | 1 | Q7PLP4;A8Y5 | Q7PLP4 | Q7PLP4 | CG41099;CG1 | |
| 0 | 1 | 1 | Q9VTI8 | Q9VTI8 | Q9VTI8 | chrb | |
| 0 | 2 | 2 | Q9VFR0 | Q9VFR0 | Q9VFR0 | CG9286 | |
| 0 | 1 | 2 | Q6IHK8 | Q6IHK8 | Q6IHK8 | HDC02276 | |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 | |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 | |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 | |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 | |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 | |

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|---|---|---|---|---|---|---|
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9VCC0 | Q9VCC0 | Q9VCC0 | CHORD |
| 0 | 1 | 1 | | REV__D4G7E | REV__D4G7E0 | |
| 0 | 2 | 2 | Q9VAA9 | Q9VAA9 | Q9VAA9 | |
| 0 | 2 | 1 | Q9W1H4 | Q9W1H4 | Q9W1H4 | DNA-ligI |
| 0 | 1 | 1 | X2JF19;Q9NB | X2JF19 | X2JF19 | hiw |
| 0 | 1 | 1 | Q8IR12;Q9VX | Q8IR12 | Q8IR12 | Cap;Cap-RA |
| 1 | 2 | 1 | Q9VZ30 | Q9VZ30 | Q9VZ30 | |
| 0 | 1 | 1 | Q9Y162 | Q9Y162 | Q9Y162 | Vps4 |
| 0 | 2 | 0 | A8DYI1;Q7K5 | A8DYI1 | A8DYI1 | CG5544 |
| 0 | 1 | 1 | Q9VIF0 | Q9VIF0 | Q9VIF0 | CG9246 |
| 0 | 1 | 0 | Q9NH11;Q9V | Q9NH11 | Q9NH11 | RecQ4 |
| 0 | 2 | 2 | T2FFB7;Q9VL | T2FFB7 | T2FFB7 | Aats-ala-RB;A |
| 0 | 2 | 1 | Q95RH7;F0JA | Q95RH7 | Q95RH7 | Rab35 |
| 0 | 1 | 0 | Q7KUA4;Q7K | Q7KUA4 | Q7KUA4 | Uba2 |
| 1 | 1 | 0 | Q9V4M2 | Q9V4M2 | Q9V4M2 | wech |
| 1 | 1 | 0 | Q9V4M2 | Q9V4M2 | Q9V4M2 | wech |
| 1 | 1 | 0 | Q9GP67;Q7K | Q9GP67 | Q9GP67 | Ret |
| 1 | 1 | 0 | D5AEK6;Q95F | D5AEK6 | D5AEK6 | CG9795-RA |
| 1 | 1 | 0 | D5AEK6;Q95F | D5AEK6 | D5AEK6 | CG9795-RA |
| 1 | 1 | 0 | Q6IKG0 | Q6IKG0 | Q6IKG0 | |
| 2 | 1 | 1 | | REV__Q8IN0 | REV__Q8IN09 | |
| 1 | 2 | 0 | Q9VWH1 | Q9VWH1 | Q9VWH1 | |
| 1 | 1 | 0 | H1UUN5;Q9V | H1UUN5 | H1UUN5 | CG14043-RA; |
| 1 | 1 | 0 | H1UUN5;Q9V | H1UUN5 | H1UUN5 | CG14043-RA; |
| 1 | 1 | 0 | Q9VR91 | Q9VR91 | Q9VR91 | HERC2 |
| 1 | 1 | 0 | Q9VIH1;Q8SX | Q9VIH1 | Q9VIH1 | RPA2;CG9273 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | A0A0B4LEV8; | A0A0B4LEV8 | A0A0B4LEV8 | coil |
| 0 | 1 | 1 | Q8IGR0;P153 | Q8IGR0 | Q8IGR0 | aru;RpS27A;R |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |

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|---|---|---|---|---|---|---|---|
| 1 | 1 | 1 | X2JDR1;Q8IR4 | X2JDR1 | X2JDR1 | CG9413-RB | |
| 1 | 1 | 1 | X2JDR1;Q8IR4 | X2JDR1 | X2JDR1 | CG9413-RB | |
| 1 | 1 | 1 | X2JDR1;Q8IR4 | X2JDR1 | X2JDR1 | CG9413-RB | |
| 1 | 1 | 1 | X2JDR1;Q8IR4 | X2JDR1 | X2JDR1 | CG9413-RB | |
| 1 | 1 | 0 | Q6IJT9 | Q6IJT9 | Q6IJT9 | HDC14233 | |
| 1 | 1 | 1 | T2GFF4 | T2GFF4 | T2GFF4 | | |
| 2 | 1 | 0 | Q9W1X7 | Q9W1X7 | Q9W1X7 | MED23 | |
| 0 | 1 | 0 | Q7KSW3 | Q7KSW3 | Q7KSW3 | | |
| 0 | 2 | 0 | Q9V3W0 | Q9V3W0 | Q9V3W0 | UK114 | |
| 1 | 1 | 1 | CON__P2093 | CON__P2093 | CON__P20930 | | |
| 1 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc;tacc-RA | |
| 1 | 1 | 0 | Q9VA95 | Q9VA95 | Q9VA95 | Bet5 | |
| 1 | 1 | 0 | B7YZZ9;P278( | B7YZZ9 | B7YZZ9 | Rrp1 | |
| 1 | 1 | 0 | B7YZZ9;P278( | B7YZZ9 | B7YZZ9 | Rrp1 | |
| 1 | 1 | 0 | B7YZZ9;P278( | B7YZZ9 | B7YZZ9 | Rrp1 | |
| 0 | 1 | 1 | Q8IHE7;C9QP | Q8IHE7 | Q8IHE7 | CG6664 | |
| 0 | 1 | 1 | Q8IHE7;C9QP | Q8IHE7 | Q8IHE7 | CG6664 | |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 2 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 0 | 1 | 2 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun | |
| 1 | 1 | 0 | Q9VGZ3;Q9N | Q9VGZ3;Q9V | Q9VGZ3 | Irp-1B;Irp-1A | |
| 0 | 1 | 2 | E1NZC8;H8F4 | E1NZC8 | E1NZC8 | MED1-RA;ME | |
| 1 | 1 | 2 | Q7KKI0;A1Z8( | Q7KKI0 | Q7KKI0 | Cct5;Cct5-RB | |
| 0 | 1 | 2 | Q9VIE7;Q8W( | Q9VIE7 | Q9VIE7 | bur | |
| 1 | 2 | 1 | | REV__A0A0B4 | REV__A0A0B4KEZ8 | | |
| 0 | 1 | 2 | Q967T2 | Q967T2 | Q967T2 | pol | |
| 0 | 1 | 0 | Q8INI3;Q86M | Q8INI3 | Q8INI3 | CG31347-RA;( | |
| 0 | 1 | 0 | Q8INI3;Q86M | Q8INI3 | Q8INI3 | CG31347-RA;( | |
| 0 | 1 | 2 | Q8IRG6;Q8IR( | Q8IRG6 | Q8IRG6 | dre4 | |
| 0 | 1 | 2 | Q8IRG6;Q8IR( | Q8IRG6 | Q8IRG6 | dre4 | |
| 0 | 1 | 2 | Q8IRG6;Q8IR( | Q8IRG6 | Q8IRG6 | dre4 | |
| 0 | 1 | 0 | Q4V3L7;Q4V3 | Q4V3L7 | Q4V3L7 | BcDNA:GH10( | |
| 0 | 1 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 | |
| 0 | 1 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 | |
| 2 | 1 | 0 | Q7KNF3;Q8IH | Q7KNF3 | Q7KNF3 | Trap1 | |
| 0 | 2 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 | |
| 0 | 2 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 | |
| 0 | 1 | 1 | A0A0B4LFL3;( | A0A0B4LFL3 | A0A0B4LFL3 | Ef1beta | |
| 1 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm | |

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|---|---|---|---|---|---|---|---|
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| | | | | | | | |
| 1 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm | |
| 0 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm | |
| 0 | 1 | 0 | Q6IGL3 | Q6IGL3 | Q6IGL3 | HDC05999 | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz | |
| 0 | 1 | 0 | A4UZZ4;Q9X1 | A4UZZ4 | A4UZZ4 | GlyP | |
| 0 | 1 | 0 | A4UZZ4;Q9X1 | A4UZZ4 | A4UZZ4 | GlyP | |
| 0 | 1 | 1 | A4UZZ4;Q9X1 | A4UZZ4 | A4UZZ4 | GlyP | |
| 0 | 1 | 1 | A4UZZ4;Q9X1 | A4UZZ4 | A4UZZ4 | GlyP | |
| 0 | 1 | 0 | Q9VY84 | Q9VY84 | Q9VY84 | | |
| 0 | 1 | 1 | A0ZWT4;A0Z' | A0ZWT4 | A0ZWT4 | TepII;Tep2 | |
| 1 | 1 | 1 | M9PBI9;M9P | M9PBI9 | M9PBI9 | sls | |
| 0 | 1 | 0 | A0A0B4JD95; | A0A0B4JD95 | A0A0B4JD95 | zip | |
| 0 | 1 | 0 | A0A0B4JD95; | A0A0B4JD95 | A0A0B4JD95 | zip | |
| 0 | 1 | 1 | Q1RKX3;A0A( | Q1RKX3 | Q1RKX3 | | |
| 1 | 1 | 0 | Q9VV82;Q8S' | Q9VV82 | Q9VV82 | CG18861;CG3 | |
| 0 | 1 | 0 | Q95RK9;Q6A: | Q95RK9 | Q95RK9 | Cap-G | |
| 0 | 1 | 0 | Q95RK9;Q6A: | Q95RK9 | Q95RK9 | Cap-G | |
| 0 | 1 | 0 | Q95RK9;Q6A: | Q95RK9 | Q95RK9 | Cap-G | |
| 0 | 1 | 0 | Q9VQ76;M9F | Q9VQ76 | Q9VQ76 | tho2 | |
| 1 | 1 | 0 | C0PUW8;Q9\ | C0PUW8 | C0PUW8 | CG3305-RA;La | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 | |
| | | | | | | | |
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|---|---|---|---|---|---|---|
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 1 | 1 | 0 | C9QPJ3;Q9VC | C9QPJ3 | C9QPJ3 | pps-RA;pps |
| 0 | 1 | 0 | | REV__Q961M | REV__Q961M1 | |
| 0 | 1 | 0 | | REV__Q961M | REV__Q961M1 | |
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |
| 0 | 1 | 1 | Q7KK51;Q9W | Q7KK51 | Q7KK51 | BcDNA.GH04 |
| 0 | 1 | 0 | M9PCD7;M9F | M9PCD7 | M9PCD7 | |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 1 | 1 | 0 | Q8MNR4 | Q8MNR4 | Q8MNR4 | gag-pol |
| 0 | 1 | 0 | O02195 | O02195 | O02195 | Trip1 |
| 0 | 1 | 0 | O02195 | O02195 | O02195 | Trip1 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |

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|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 1 | 1 | 0 | B9ER03 | B9ER03 | B9ER03 | CG10597-RB |
| 0 | 1 | 0 | Q4AB54;P022 | Q4AB54 | Q4AB54 | His1:CG3386 |
| 0 | 1 | 0 | Q4AB54;P022 | Q4AB54 | Q4AB54 | His1:CG3386 |
| 0 | 1 | 0 | Q4AB54;P022 | Q4AB54 | Q4AB54 | His1:CG3386 |
| 0 | 4 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | |
| 0 | 1 | 0 | Q95RN0-2 | Q95RN0-2 | Q95RN0-2 | CG10038 |
| 0 | 1 | 0 | Q9VZS3 | Q9VZS3 | Q9VZS3 | CG17737 |
| 0 | 1 | 0 | Q9VZS3 | Q9VZS3 | Q9VZS3 | CG17737 |
| 0 | 1 | 0 | Q8INM3;Q8IN | Q8INM3 | Q8INM3 | sle |
| 0 | 1 | 0 | Q8INM3;Q8IN | Q8INM3 | Q8INM3 | sle |
| 1 | 2 | 1 | A0A0H4Y1G5 | A0A0H4Y1G5 | A0A0H4Y1G5 | hyd |
| 2 | 2 | 1 | A0A0H4Y1G5 | A0A0H4Y1G5 | A0A0H4Y1G5 | hyd |
| 2 | 2 | 1 | A0A0H4Y1G5 | A0A0H4Y1G5 | A0A0H4Y1G5 | hyd |
| 0 | 2 | 2 | Q9VPR5;Q4V | Q9VPR5 | Q9VPR5 | CG2807 |
| 1 | 1 | 0 | Q9W5W8 | Q9W5W8 | Q9W5W8 | |
| 0 | 1 | 0 | Q9W401 | Q9W401 | Q9W401 | kdn |
| 0 | 1 | 0 | Q9XZL7;A0A0 | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0A0 | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0A0 | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0A0 | Q9XZL7 | Q9XZL7 | tacc |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc | |
| 0 | 2 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc | |
| 0 | 2 | 0 | M9PDK5;Q9V | M9PDK5 | M9PDK5 | VhaSFD | |
| 0 | 1 | 2 | Q4V3Z6 | Q4V3Z6 | Q4V3Z6 | | |
| 0 | 2 | 0 | A0A0C5K8A0 | A0A0C5K8A0 | A0A0C5K8A0 | lds | |
| 0 | 2 | 1 | M9NDM4;Q9 | M9NDM4 | M9NDM4 | wds | |
| 0 | 1 | 0 | Q86BJ3-3 | Q86BJ3-3 | Q86BJ3-3 | | |
| 0 | 1 | 0 | P81900;A8DY | P81900 | P81900 | Pka-R2 | |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 | |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 | |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 | |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 | |
| 0 | 2 | 2 | Q9VBX4 | Q9VBX4 | Q9VBX4 | CG31510-RA | |
| 0 | 1 | 2 | C7LAH9;C9QF | C7LAH9 | C7LAH9 | Moe;Moe-RA | |
| 0 | 2 | 2 | Q967T2 | Q967T2 | Q967T2 | pol | |
| 0 | 1 | 0 | A1Z968;Q5KT | A1Z968 | A1Z968 | NAT1 | |
| 0 | 3 | 0 | Q9VKW5 | Q9VKW5 | Q9VKW5 | | |
| 0 | 1 | 0 | Q29QZ8 | Q29QZ8 | Q29QZ8 | | |
| 1 | 1 | 0 | Q9VIS5 | Q9VIS5 | Q9VIS5 | | |
| 0 | 2 | 2 | A8E774;P250 | A8E774 | A8E774 | Cyp1;CG9916 | |
| 0 | 1 | 2 | Q9W335 | Q9W335 | Q9W335 | l(1)G0320 | |
| 0 | 1 | 2 | Q9W335 | Q9W335 | Q9W335 | l(1)G0320 | |
| 0 | 2 | 1 | A1A6R3;Q9VI | A1A6R3 | A1A6R3 | | |
| 0 | 1 | 1 | Q9VWF8 | Q9VWF8 | Q9VWF8 | | |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 | |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 | |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 | |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote | |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote | |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote | |
| 0 | 1 | 1 | A0A0B4K7G4 | A0A0B4K7G4 | A0A0B4K7G4 | mod | |
| 0 | 1 | 0 | Q9VL18 | Q9VL18 | Q9VL18 | eEF1delta | |
| 0 | 1 | 0 | Q9VL18 | Q9VL18 | Q9VL18 | eEF1delta | |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon | |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon | |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon | |
| 0 | 1 | 1 | Q9W384;Q9E | Q9W384 | Q9W384 | dalao | |
| 1 | 1 | 1 | X2JIN0;M9M | X2JIN0 | X2JIN0 | | |
| 0 | 2 | 2 | Q24574-2;Q2 | Q24574-2 | Q24574-2 | Ubp64E | |
| 0 | 2 | 2 | Q24574-2;Q2 | Q24574-2 | Q24574-2 | Ubp64E | |
| 0 | 1 | 1 | A0A0B4K7Z5; | A0A0B4K7Z5 | A0A0B4K7Z5 | Rpn6 | |
| 0 | 1 | 0 | M9PFS8;Q9V | M9PFS8 | M9PFS8 | CG9705 | |
| 0 | 1 | 0 | M9PFS8;Q9V | M9PFS8 | M9PFS8 | CG9705 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0 | 2 | 0 | B7Z0G1;Q02 | B7Z0G1 | B7Z0G1 | hay | |
| 1 | 1 | 1 | CON__P0266 | CON__P0266 | CON__P02662 | | |
| 1 | 1 | 1 | CON__P0266 | CON__P0266 | CON__P02662 | | |
| 0 | 1 | 0 | Q9VE98 | Q9VE98 | Q9VE98 | | |
| 0 | 1 | 0 | Q9VE98 | Q9VE98 | Q9VE98 | | |
| 0 | 1 | 0 | Q9VIS5 | Q9VIS5 | Q9VIS5 | | |
| 0 | 2 | 1 | Q9V3U0 | Q9V3U0 | Q9V3U0 | CG4500 | |
| 0 | 1 | 1 | E1JI68 | E1JI68 | E1JI68 | | |
| 0 | 1 | 1 | Q9VRV7 | Q9VRV7 | Q9VRV7 | CG13298 | |
| 0 | 1 | 0 | Q8MSA2;Q8M | Q8MSA2 | Q8MSA2 | CG14730 | |
| 0 | 1 | 0 | Q9VPW4 | Q9VPW4 | Q9VPW4 | mtRNApol | |
| 1 | 1 | 1 | A1ZBT6;Q96C | A1ZBT6 | A1ZBT6 | | |

| Protein Name | Type | Labeling State | Raw file | Fraction | Experiment | MS/MS m/z |
|---|---|---|---|---|---|---|
| Zinc finger pr | MULTI-MSMS | | PT5722-2 | 2 | B1 | 761.34 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 761.67 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 735.02 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 734.69 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 777.72 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 777.38 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 804.37 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 804.38 |
| 1 | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 767.35 |
| Polycomb prc | ISO-MSMS | 1 | PT5722-40 | 40 | B3 SCX | 913.44 |
| 26S proteaso | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 631.25 |
| Hsc70-intera | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 516.59 |
| Hsc70-intera | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 774.39 |
| ‹e-RA | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 757.02 |
| Odorant bind | MSMS | 1 | PT5722-3 | 3 | B1 | 753.86 |
| | MSMS | 1 | PT5722-19 | 19 | B2 | 753.85 |
| Multidrug-re | MSMS | 1 | PT5722-48 | 48 | H/H | 489.94 |
| Phosphogluc | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 782.38 |
| Phosphogluc | MULTI-MSMS | | PT5722-8 | 8 | B1 SCX | 782.38 |
| Phosphogluc | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 782.05 |
| Phosphogluc | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 782.38 |
| Phosphogluc | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 782.38 |
| Phosphogluc | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 1173.07 |
| Phosphogluc | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 782.05 |
| Phosphogluc | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 782.05 |
| Phosphogluc | MULTI-MATCH | | PT5722-6 | 6 | B1 SCX | |
| Phosphogluc | MULTI-MATCH | | PT5722-21 | 21 | B2 SCX | |
| Phosphogluc | MULTI-MATCH | | PT5722-22 | 22 | B2 SCX | |
| Phosphogluc | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 782.71 |
| Protein purity | MSMS | 1 | PT5722-32 | 32 | B3 | 687.36 |
| Glycogen [sta | MULTI-MSMS | | PT5722-2 | 2 | B1 | 1106.52 |
| Glycogen [sta | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 1106.02 |
| Glycogen [sta | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 1106.03 |
| Glycogen [sta | MULTI-MSMS | | PT5722-47 | 47 | H/H | 1106.52 |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1106.52 |
| Glycogen [sta | MULTI-MATCH | | PT5722-56 | 56 | H/H TIO2 | |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1146.5 |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 764.67 |
| Tripeptidyl-p | ISO-MSMS | 0 | PT5722-6 | 6 | B1 SCX | 943.2 |
| Tripeptidyl-p | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 943.2 |
| Tripeptidyl-p | ISO-MSMS | 0 | PT5722-21 | 21 | B2 SCX | 943.2 |
| Tripeptidyl-p | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 943.2 |

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| Tripeptidyl-p | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 942.95 |
| Transcription | MULTI-MSMS | | PT5722-1 | 1 | B1 | 812.4 |
| | MULTI-MSMS | | PT5722-3 | 3 | B1 | 954.97 |
| | MULTI-SECPEP | | PT5722-3 | 3 | B1 | 954.97 |
| | MULTI-MATCH | | PT5722-2 | 2 | B1 | |
| Ubiquitin-cor | MULTI-MSMS | | PT5722-20 | 20 | B2 | 862.37 |
| | MSMS | 1 | PT5722-19 | 19 | B2 | 547.28 |
| | MSMS | 1 | PT5722-20 | 20 | B2 | 547.28 |
| | MSMS | 1 | PT5722-6 | 6 | B1 SCX | 956.93 |
| | MSMS | 1 | PT5722-6 | 6 | B1 SCX | 956.93 |
| | MSMS | 1 | PT5722-7 | 7 | B1 SCX | 956.93 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-2 | 2 | B1 | 841.84 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-6 | 6 | B1 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-11 | 11 | B1 TIO2 | 841.34 |
| Eukaryotic tra | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 841.34 |
| Eukaryotic tra | ISO-MSMS | 0 | PT5722-27 | 27 | B2 TIO2 | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 841.33 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-41 | 41 | B3 TIO2 | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 841.83 |
| Eukaryotic tra | MULTI-MATCH | | PT5722-42 | 42 | B3 TIO2 | |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-5 | 5 | B1 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-15 | 15 | B1 TIO2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-16 | 16 | B2 | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-20 | 20 | B2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-30 | 30 | B2 TIO2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-32 | 32 | B3 | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-34 | 34 | B3 | 622.76 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-49 | 49 | H/H | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-50 | 50 | H/H | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-60 | 60 | H/H TIO2 | 622.76 |
| Cofilin/actin-( | MULTI-MATCH | | PT5722-33 | 33 | B3 | |
| | MSMS | 1 | PT5722-48 | 48 | H/H | 729.36 |
| NADH-ubiqui | ISO-MSMS | 1 | PT5722-7 | 7 | B1 SCX | 817.71 |
| 1,2-dihydrox | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 659.82 |
| 1,2-dihydrox | MULTI-MATCH | | PT5722-52 | 52 | H/H SCX | |
| | MULTI-MSMS | | PT5722-8 | 8 | B1 SCX | 619.25 |
| | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 619.25 |
| Protein split e | MSMS | 0 | PT5722-18 | 18 | B2 | 671.34 |
| | ISO-MSMS | 1 | PT5722-24 | 24 | B2 SCX | 774.37 |
| FACT comple | ISO-MSMS | 0 | PT5722-6 | 6 | B1 SCX | 822.02 |

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| FACT comple: | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 821.69 |
| FACT comple: | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 822.02 |
| Akap200 | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 905.41 |
| Probable pho | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 388.19 |
| Probable pho | MULTI-SECPEP | | PT5722-37 | 37 | B3 SCX | 388.46 |
| Putative gust | MULTI-MSMS | | PT5722-8 | 8 | B1 SCX | 926.9 |
| Bifunctional g | ISO-MSMS | 0 | PT5722-21 | 21 | B2 SCX | 909.75 |
| Bifunctional g | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 909.75 |
| Bifunctional g | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 909.75 |
| | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 741.37 |
| Gelsolin | ISO-MSMS | 1 | PT5722-18 | 18 | B2 | 684.32 |
| | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 788.38 |
| | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 1052.44 |
| | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 1052.78 |
| | ISO-MSMS | 0 | PT5722-53 | 53 | H/H SCX | 1052.78 |
| | MSMS | 0 | PT5722-48 | 48 | H/H | 901.94 |
| | ISO-MSMS | 0 | PT5722-5 | 5 | B1 | 812.36 |
| Dipeptidyl pe | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 542.93 |
| | MSMS | 0 | PT5722-28 | 28 | B2 TIO2 | 697.72 |
| 4D | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 612.8 |
| 39S ribosoma | MULTI-MSMS | | PT5722-34 | 34 | B3 | 786.04 |
| | ISO-MSMS | 1 | PT5722-4 | 4 | B1 | 791.04 |
| DNA-directed | MSMS | 1 | PT5722-39 | 39 | B3 SCX | 847.09 |
| | ISO-MSMS | 1 | PT5722-40 | 40 | B3 SCX | 919.1 |
| Heat shock pı | MULTI-MSMS | | PT5722-17 | 17 | B2 | 730.78 |
| | ISO-MSMS | 1 | PT5722-10 | 10 | B1 SCX | 707.27 |
| | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 707.27 |
| | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 702.76 |
| | MSMS | 0 | PT5722-1 | 1 | B1 | 948.6 |
| | MSMS | 0 | PT5722-49 | 49 | H/H | 500.9 |
| | MSMS | 0 | PT5722-39 | 39 | B3 SCX | 841.88 |
| | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 642.3 |
| | MULTI-MSMS | | PT5722-48 | 48 | H/H | 642.3 |
| | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 642.31 |
| | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 693.37 |
| | MSMS | 1 | PT5722-48 | 48 | H/H | 906.45 |
| Pyruvate carb | MULTI-SECPEP | | PT5722-37 | 37 | B3 SCX | 620.84 |
| | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 821.74 |
| | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 821.74 |
| Cyclin-depen | MULTI-MSMS | | PT5722-34 | 34 | B3 | 633.29 |

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| | MULTI-MSMS | | PT5722-3 | 3 | B1 | 792.38 |
| | MULTI-MSMS | | PT5722-18 | 18 | B2 | 789.36 |
| | MSMS | 0 | PT5722-22 | 22 | B2 SCX | 1287.06 |
| | MULTI-SECPEP | | PT5722-3 | 3 | B1 | 913.45 |
| | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 908.94 |
| | MULTI-MATCH | | PT5722-2 | 2 | B1 | |
| | MULTI-MATCH | | PT5722-38 | 38 | B3 SCX | |
| | MULTI-MATCH | | PT5722-40 | 40 | B3 SCX | |
| | MULTI-MSMS | | PT5722-10 | 10 | B1 SCX | 837.71 |
| | MULTI-SECPEP | | PT5722-10 | 10 | B1 SCX | 837.71 |
| | ISO-MSMS | 1 | PT5722-7 | 7 | B1 SCX | 924.41 |
| Titin | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 864.91 |
| Titin | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 864.91 |
| Titin | MSMS | 0 | PT5722-37 | 37 | B3 SCX | 856.91 |
| Poly [ADP-rib | MULTI-SECPEP | | PT5722-48 | 48 | H/H | 713.99 |
| )15-RB | ISO-MSMS | 0 | PT5722-5 | 5 | B1 | 911.95 |
| Longitudinals | ISO-MSMS | 0 | PT5722-10 | 10 | B1 SCX | 721.68 |
| Heat shock 7( | MSMS | 0 | PT5722-32 | 32 | B3 | 496.93 |
| 60S acidic rib | MULTI-MSMS | | PT5722-25 | 25 | B2 SCX | 1037.38 |
| 60S acidic rib | ISO-MSMS | 0 | PT5722-45 | 45 | B3 TIO2 | 1037.38 |
| 60S acidic rib | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 1037.38 |
| Zinc finger pr | MSMS | 1 | PT5722-8 | 8 | B1 SCX | 491.23 |
| Heterochrom | ISO-MSMS | 0 | PT5722-9 | 9 | B1 SCX | 727.32 |
| Heterochrom | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 969.42 |
| Heterochrom | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 727.32 |
| Heterochrom | ISO-MSMS | 0 | PT5722-54 | 54 | H/H SCX | 727.32 |
| | ISO-MSMS | 0 | PT5722-10 | 10 | B1 SCX | 854.39 |
| | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 854.39 |
| 60S acidic rib | MSMS | 0 | PT5722-6 | 6 | B1 SCX | 1184.42 |
| 60S acidic rib | MSMS | 0 | PT5722-36 | 36 | B3 SCX | 789.95 |
| 60S acidic rib | MSMS | 0 | PT5722-40 | 40 | B3 SCX | 789.95 |
| 60S acidic rib | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 763.63 |
| Cysteine and | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 732.32 |
| | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 728.65 |
| 17419 | ISO-MSMS | 1 | PT5722-23 | 23 | B2 SCX | 671.36 |
| Protein chary | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 847.4 |
| Protein BCCIP | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 915.96 |
| | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 714.86 |
| Protein NASP | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 632.94 |
| Protein NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 632.61 |
| Protein NASP | MULTI-MSMS | | PT5722-32 | 32 | B3 | 632.61 |
| Protein NASP | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 632.94 |
| Protein NASP | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 632.61 |

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| Protein NASP | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 632.61 |
| Cysteine and | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 1033.93 |
| | MULTI-MSMS | | PT5722-32 | 32 | B3 | 758.05 |
| | ISO-MSMS | 0 | PT5722-55 | 55 | H/H SCX | 765.87 |
| DNA ligase 1 | ISO-MSMS | 1 | PT5722-27 | 27 | B2 TIO2 | 790.89 |
| E3 ubiquitin-p | MSMS | 0 | PT5722-54 | 54 | H/H SCX | 586.95 |
| | MULTI-MSMS | | PT5722-33 | 33 | B3 | 739.02 |
| | ISO-MSMS | 1 | PT5722-34 | 34 | B3 | 968.12 |
| | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 777.4 |
| | MULTI-SECPEP | | PT5722-48 | 48 | H/H | 905.45 |
| Nucleolar cor | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 1108.79 |
| | ISO-MSMS | 0 | PT5722-35 | 35 | B3 | 758.35 |
| Alanine--tRNA | MSMS | 1 | PT5722-3 | 3 | B1 | 990.81 |
| | MSMS | 0 | PT5722-18 | 18 | B2 | 690.97 |
| | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 468.23 |
| Protein wech | ISO-MSMS | 0 | PT5722-8 | 8 | B1 SCX | 991.94 |
| Protein wech | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 991.94 |
| | MSMS | 0 | PT5722-38 | 38 | B3 SCX | 764.41 |
| | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 567.61 |
| | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 850.9 |
| | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 835.39 |
| | ISO-MSMS | 1 | PT5722-34 | 34 | B3 | 913.48 |
| | MULTI-MSMS | | PT5722-10 | 10 | B1 SCX | 745.02 |
| Protein KBP h | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 859.41 |
| Protein KBP h | MULTI-MATCH | | PT5722-37 | 37 | B3 SCX | |
| Probable E3 u | MULTI-MSMS | | PT5722-33 | 33 | B3 | 760.74 |
| | MULTI-MSMS | | PT5722-34 | 34 | B3 | 837.68 |
| | ISO-MSMS | 1 | PT5722-23 | 23 | B2 SCX | 818.4 |
| | ISO-MSMS | 1 | PT5722-24 | 24 | B2 SCX | 818.4 |
| | ISO-MSMS | 1 | PT5722-38 | 38 | B3 SCX | 817.9 |
| | ISO-MSMS | 1 | PT5722-49 | 49 | H/H | 817.9 |
| | MULTI-MSMS | | PT5722-33 | 33 | B3 | 632.61 |
| Ubiquitin-40S | MSMS | 0 | PT5722-16 | 16 | B2 | 694.8 |
| | MULTI-MSMS | | PT5722-10 | 10 | B1 SCX | 909.43 |
| | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 609.63 |
| | MULTI-MATCH | | PT5722-23 | 23 | B2 SCX | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 597.63 |
| | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 896.44 |
| | MULTI-MATCH | | PT5722-23 | 23 | B2 SCX | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| sobremesa | ISO-MSMS | 1 | PT5722-8 | 8 | B1 SCX | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-9 | 9 | B1 SCX | 911.43 |

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| sobremesa | ISO-MSMS | 1 | PT5722-10 | 10 | B1 SCX | 911.44 |
| sobremesa | ISO-MSMS | 1 | PT5722-26 | 26 | B2 TIO2 | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-38 | 38 | B3 SCX | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-40 | 40 | B3 SCX | 911.44 |
| | ISO-MSMS | 0 | PT5722-49 | 49 | H/H | 793.86 |
| | ISO-MSMS | 0 | PT5722-35 | 35 | B3 | 801.37 |
| Mediator of F | ISO-MSMS | 0 | PT5722-53 | 53 | H/H SCX | 824.38 |
| | ISO-MSMS | 0 | PT5722-52 | 52 | H/H SCX | 905.45 |
| | MULTI-SECPEP | | PT5722-10 | 10 | B1 SCX | 497.28 |
| | ISO-MSMS | 1 | PT5722-38 | 38 | B3 SCX | 830.09 |
| | ISO-MSMS | 0 | PT5722-41 | 41 | B3 TIO2 | 930.46 |
| | MULTI-SECPEP | | PT5722-10 | 10 | B1 SCX | 750.85 |
| Recombinatic | ISO-MSMS | 0 | PT5722-12 | 12 | B1 TIO2 | 914.74 |
| Recombinatic | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 914.41 |
| Recombinatic | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 914.74 |
| | ISO-MSMS | 1 | PT5722-10 | 10 | B1 SCX | 635.32 |
| | ISO-MSMS | 1 | PT5722-55 | 55 | H/H SCX | 634.82 |
| | MULTI-MSMS | | PT5722-2 | 2 | B1 | 555.27 |
| | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 832.41 |
| | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 555.27 |
| | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 832.4 |
| | MULTI-MATCH | | PT5722-36 | 36 | B3 SCX | |
| | MULTI-MSMS | | PT5722-2 | 2 | B1 | 597.97 |
| | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 597.97 |
| | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 694.33 |
| Mediator of F | MSMS | 0 | PT5722-3 | 3 | B1 | 719.36 |
| | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 766.07 |
| | MSMS | 0 | PT5722-38 | 38 | B3 SCX | 883.43 |
| | ISO-MSMS | 1 | PT5722-4 | 4 | B1 | 799.37 |
| | ISO-MSMS | 1 | PT5722-3 | 3 | B1 | 799.4 |
| CG31347 | MULTI-MSMS | | PT5722-33 | 33 | B3 | 482.89 |
| CG31347 | MULTI-MATCH | | PT5722-34 | 34 | B3 | |
| FACT comple | MULTI-MSMS | | PT5722-21 | 21 | B2 SCX | 754.67 |
| FACT comple | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 754.33 |
| FACT comple | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 754.33 |
| 614;BcDNA.GI | ISO-MSMS | -1 | PT5722-35 | 35 | B3 | 563.71 |
| smallish, sma | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 558.59 |
| smallish, sma | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 558.58 |
| | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 936.46 |
| smallish, sma | MULTI-SECPEP | | PT5722-16 | 16 | B2 | 958.48 |
| smallish, sma | MULTI-SECPEP | | PT5722-33 | 33 | B3 | 958.48 |
| Probable elor | ISO-MSMS | 0 | PT5722-24 | 24 | B2 SCX | 926.15 |
| | MULTI-MSMS | | PT5722-20 | 20 | B2 | 615.25 |

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| | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 615.25 |
| | MULTI-MSMS | | PT5722-50 | 50 | H/H | 602.75 |
| | MULTI-SECPEP | | PT5722-50 | 50 | H/H | 425.52 |
| | ISO-MSMS | 0 | PT5722-6 | 6 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-8 | 8 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-19 | 19 | B2 | 678.86 |
| | ISO-MSMS | 0 | PT5722-20 | 20 | B2 | 678.86 |
| | ISO-MSMS | 0 | PT5722-21 | 21 | B2 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-24 | 24 | B2 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-31 | 31 | B3 | 678.86 |
| | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 678.86 |
| | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-46 | 46 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-47 | 47 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-50 | 50 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-54 | 54 | H/H SCX | 678.86 |
| Phosphorylas | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 931.47 |
| Phosphorylas | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 931.98 |
| Phosphorylas | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 664.02 |
| Phosphorylas | MULTI-MATCH | | PT5722-36 | 36 | B3 SCX | |
| | MULTI-MSMS | | PT5722-25 | 25 | B2 SCX | 589.8 |
| | MSMS | 0 | PT5722-38 | 38 | B3 SCX | 707.81 |
| Titin | MSMS | 1 | PT5722-8 | 8 | B1 SCX | 806.39 |
| Myosin heavy | ISO-MSMS | 0 | PT5722-10 | 10 | B1 SCX | 613.29 |
| Myosin heavy | ISO-MSMS | 0 | PT5722-55 | 55 | H/H SCX | 613.29 |
| | ISO-MSMS | 0 | PT5722-4 | 4 | B1 | 689.38 |
| 32164-RA | ISO-MSMS | 1 | PT5722-25 | 25 | B2 SCX | 613.28 |
| | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 814.89 |
| | ISO-MSMS | 0 | PT5722-50 | 50 | H/H | 814.89 |
| | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 814.89 |
| | MULTI-SECPEP | | PT5722-19 | 19 | B2 | 908.98 |
| amp1 | MULTI-MSMS | | PT5722-35 | 35 | B3 | 620.77 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-8 | 8 | B1 SCX | 717.63 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 717.3 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-33 | 33 | B3 | 717.63 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 717.63 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-40 | 40 | B3 SCX | 717.63 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-48 | 48 | H/H | 720.63 |

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|---|---|---|---|---|---|---|---|---|
| Vitellogenin-1 | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 717.29 | | |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-55 | 55 | H/H SCX | 717.63 | | |
| | MULTI-MSMS | | PT5722-4 | 4 | B1 | 990.98 | | |
| | MULTI-MSMS | | PT5722-18 | 18 | B2 | 990.98 | | |
| | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 990.98 | | |
| | MULTI-MATCH | | PT5722-24 | 24 | B2 SCX | | | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | | | |
| | MULTI-MSMS | | PT5722-33 | 33 | B3 | 887.1 | | |
| | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 715.84 | | |
| | MULTI-MATCH | | PT5722-54 | 54 | H/H SCX | | | |
| Survival motc | ISO-MSMS | 0 | PT5722-24 | 24 | B2 SCX | 1072.48 | | |
| Survival motc | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 1072.47 | | |
| Survival motc | ISO-MSMS | 0 | PT5722-40 | 40 | B3 SCX | 1072.47 | | |
| | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 753.05 | | |
| | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 752.72 | | |
| | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 753.05 | | |
| 31367-RA | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 670.97 | | |
| 31367-RA | MULTI-MATCH | | PT5722-21 | 21 | B2 SCX | | | |
| 31367-RA | MULTI-MATCH | | PT5722-22 | 22 | B2 SCX | | | |
| 637;BcDNA:GI | MSMS | 0 | PT5722-24 | 24 | B2 SCX | 469.58 | | |
| | MSMS | 0 | PT5722-49 | 49 | H/H | 629.31 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 727.67 | | |
| Protein NASP | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 546.01 | | |
| Protein NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 727.68 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 545.76 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 546.01 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 545.76 | | |
| Protein NASP | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 728.01 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 546.01 | | |
| Protein NASP | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 727.68 | | |
| | ISO-MSMS | 0 | PT5722-35 | 35 | B3 | 953.43 | | |
| Eukaryotic tra | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 1016.01 | | |
| Eukaryotic tra | MULTI-MATCH | | PT5722-37 | 37 | B3 SCX | | | |
| Akap200 | ISO-MSMS | 0 | PT5722-9 | 9 | B1 SCX | | 738 | |
| Akap200 | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 737.66 | | |
| Akap200 | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 737.67 | | |
| Akap200 | ISO-MSMS | 0 | PT5722-47 | 47 | H/H | 737.66 | | |
| Akap200 | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 743.68 | | |
| Protein NASP | MULTI-MSMS | | PT5722-3 | 3 | B1 | 1029.47 | | |
| Protein NASP | MULTI-MSMS | | PT5722-12 | 12 | B1 TIO2 | 1028.97 | | |
| Protein NASP | MULTI-MSMS | | PT5722-13 | 13 | B1 TIO2 | 1028.97 | | |
| Protein NASP | MULTI-MSMS | | PT5722-14 | 14 | B1 TIO2 | 1028.97 | | |
| Protein NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 1029.47 | | |

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|---|---|---|---|---|---|---|
| Protein NASP | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 1028.97 |
| Protein NASP | MULTI-MSMS | | PT5722-27 | 27 | B2 TIO2 | 1028.97 |
| Protein NASP | MULTI-MSMS | | PT5722-28 | 28 | B2 TIO2 | 1028.97 |
| Protein NASP | MULTI-MSMS | | PT5722-29 | 29 | B2 TIO2 | 1028.97 |
| Protein NASP | MULTI-MSMS | | PT5722-32 | 32 | B3 | 1029.47 |
| Protein NASP | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 686.65 |
| Protein NASP | MULTI-MSMS | | PT5722-33 | 33 | B3 | 1028.97 |
| Protein NASP | MULTI-MSMS | | PT5722-33 | 33 | B3 | 686.32 |
| Protein NASP | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 1028.98 |
| Protein NASP | MULTI-MSMS | | PT5722-42 | 42 | B3 TIO2 | 1033.48 |
| Protein NASP | MULTI-MSMS | | PT5722-42 | 42 | B3 TIO2 | 686.65 |
| Protein NASP | MULTI-MSMS | | PT5722-43 | 43 | B3 TIO2 | 1029.47 |
| Protein NASP | MULTI-MSMS | | PT5722-44 | 44 | B3 TIO2 | 1028.96 |
| Protein NASP | ISO-MSMS | 0 | PT5722-44 | 44 | B3 TIO2 | 686.65 |
| Protein NASP | ISO-MSMS | 0 | PT5722-45 | 45 | B3 TIO2 | 1028.98 |
| Protein NASP | MULTI-MSMS | | PT5722-47 | 47 | H/H | 1029.47 |
| Protein NASP | MULTI-MSMS | | PT5722-48 | 48 | H/H | 1028.96 |
| Protein NASP | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 1028.96 |
| Protein NASP | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1029.47 |
| Protein NASP | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 1028.97 |
| Protein NASP | MSMS | 0 | PT5722-58 | 58 | H/H TIO2 | 686.32 |
| Protein NASP | MULTI-MSMS | | PT5722-59 | 59 | H/H TIO2 | 1028.97 |
| Protein NASP | MULTI-MATCH | | PT5722-2 | 2 | B1 | |
| | MULTI-MSMS | | PT5722-4 | 4 | B1 | 671.68 |
| Histone H1 | ISO-MSMS | 0 | PT5722-4 | 4 | B1 | 693.66 |
| Histone H1 | ISO-MSMS | 0 | PT5722-19 | 19 | B2 | 1039.49 |
| Histone H1 | MULTI-MSMS | | PT5722-49 | 49 | H/H | 693.33 |
| | MSMS | 1 | PT5722-23 | 23 | B2 SCX | 732.71 |
| UPF0528 pro | ISO-MSMS | 0 | PT5722-14 | 14 | B1 TIO2 | 700.65 |
| Protein trans | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 963.46 |
| Protein trans | ISO-MSMS | 0 | PT5722-45 | 45 | B3 TIO2 | 963.47 |
| Protein slend | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 845.37 |
| Protein slend | MULTI-MATCH | | PT5722-58 | 58 | H/H TIO2 | |
| E3 ubiquitin-p | MULTI-MSMS | | PT5722-19 | 19 | B2 | 785.71 |
| E3 ubiquitin-p | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 791.04 |
| E3 ubiquitin-p | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| | ISO-MSMS | 0 | PT5722-12 | 12 | B1 TIO2 | 844.38 |
| | MSMS | 1 | PT5722-33 | 33 | B3 | 655.32 |
| Probable citra | MULTI-SECPEP | | PT5722-23 | 23 | B2 SCX | 608.32 |
| tacc | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 826.91 |
| | MULTI-MSMS | | PT5722-41 | 41 | B3 TIO2 | 826.91 |
| | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 826.9 |
| | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 826.9 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 826.4 |
| | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 866.39 |
| V-type proto | MSMS | 1 | PT5722-31 | 31 | B3 | 895.9 |
| | MSMS | 1 | PT5722-38 | 38 | B3 SCX | 679.38 |
| Transcription | MSMS | 0 | PT5722-56 | 56 | H/H TIO2 | 755.73 |
| Protein will d | MSMS | 0 | PT5722-49 | 49 | H/H | 749.34 |
| | ISO-MSMS | 1 | PT5722-4 | 4 | B1 | 982.46 |
| cAMP-depen | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 876.03 |
| Nedd8-activa | MULTI-MSMS | | PT5722-11 | 11 | B1 TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-28 | 28 | B2 TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 799.9 |
| | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 988.49 |
| Moesin/ezrin | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 410.24 |
| | MSMS | 0 | PT5722-34 | 34 | B3 | 696.01 |
| | MULTI-MSMS | | PT5722-2 | 2 | B1 | 861.78 |
| | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 1073.18 |
| | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 717.84 |
| | MULTI-SECPEP | | PT5722-22 | 22 | B2 SCX | 926.46 |
| Peptidyl-prol | ISO-MSMS | 1 | PT5722-39 | 39 | B3 SCX | 747.37 |
| | MULTI-MSMS | | PT5722-19 | 19 | B2 | 440.23 |
| | MULTI-MSMS | | PT5722-34 | 34 | B3 | 440.56 |
| | ISO-MSMS | 1 | PT5722-39 | 39 | B3 SCX | 988.48 |
| | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 651.83 |
| Probable hist | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 1008.44 |
| Probable hist | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 1008.44 |
| Probable hist | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 1008.77 |
| Otefin | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 954.95 |
| Otefin | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 954.96 |
| Otefin | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 954.96 |
| DNA-binding | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 588.95 |
| Probable elor | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 628.31 |
| Probable elor | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 627.97 |
| | MULTI-MSMS | | PT5722-4 | 4 | B1 | 672.02 |
| | MULTI-MSMS | | PT5722-18 | 18 | B2 | 672.02 |
| | MULTI-MSMS | | PT5722-32 | 32 | B3 | 671.69 |
| Bap111 Brahı | ISO-MSMS | 0 | PT5722-34 | 34 | B3 | 903.72 |
| | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 622.65 |
| Ubiquitin carl | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 766.07 |
| Ubiquitin carl | MULTI-MATCH | | PT5722-36 | 36 | B3 SCX | |
| 26S proteaso | MSMS | 0 | PT5722-48 | 48 | H/H | 623.31 |
| Cold shock dc | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 767.82 |
| Cold shock dc | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 772.32 |

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|---|---|---|---|---|---|---|
| DNA excision | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 874.37 |
| | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 641.82 |
| | ISO-MSMS | 0 | PT5722-48 | 48 | H/H | 642.07 |
| | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 671.85 |
| | MULTI-MATCH | | PT5722-36 | 36 | B3 SCX | |
| | MSMS | 0 | PT5722-20 | 20 | B2 | 705.34 |
| Long-chain-fa | ISO-MSMS | 0 | PT5722-54 | 54 | H/H SCX | 720.38 |
| | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 738.86 |
| Splicing facto | ISO-MSMS | 0 | PT5722-52 | 52 | H/H SCX | 557.25 |
| | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 710.36 |
| DNA-directed | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 821.92 |
| | ISO-MSMS | 1 | PT5722-39 | 39 | B3 SCX | 918.1 |

| Charge | m/z | Mass | Resolution | Uncalibrated | Uncalibrated | Mass Error [p |
|---|---|---|---|---|---|---|
| 3 | 761341567 | 228100287 | 48700.75 | -0.6341 | -0.00048276 | -0.040968 |
| 3 | 761341567 | 228100287 | NaN | NaN | NaN | 0.14489 |
| 3 | 734686124 | 220103654 | NaN | NaN | NaN | 0.91062 |
| 3 | 734686124 | 220103654 | NaN | NaN | NaN | 0.23012 |
| 3 | 777384445 | 23291315 | NaN | NaN | NaN | 0.8582 |
| 3 | 777384445 | 23291315 | NaN | NaN | NaN | 0.78236 |
| 3 | 804039888 | 240909784 | NaN | NaN | NaN | 0.47731 |
| 3 | 804039888 | 240909784 | NaN | NaN | NaN | 0.28295 |
| 3 | 767354045 | 229904031 | 48876.38 | 0 | 0 | -10011 |
| 2 | 908936794 | 181585904 | NaN | NaN | NaN | 13756 |
| 2 | 631254526 | 12604945 | NaN | NaN | NaN | -0.29455 |
| 3 | 516592108 | 154675449 | 56958.66 | 0.15225 | 0.78649 | -0.58953 |
| 2 | 774384523 | 154675449 | 48267.14 | -0.51862 | -0.00040161 | -0.68776 |
| 3 | 757022497 | 226804566 | NaN | NaN | NaN | -0.17349 |
| 2 | 749842461 | 149767037 | NaN | NaN | NaN | NaN |
| 2 | 749842461 | 149767037 | NaN | NaN | NaN | NaN |
| 3 | 484593449 | 145075852 | NaN | NaN | NaN | NaN |
| 3 | 782049285 | 234312603 | 49084.29 | -0.31035 | -0.00024271 | -0.22733 |
| 3 | 782049285 | 234312603 | 47136.54 | -0.6614 | -0.00051725 | -0.84304 |
| 3 | 782049285 | 234312603 | 48041.27 | -0.65958 | -0.00051582 | -0.34588 |
| 3 | 782049285 | 234312603 | NaN | NaN | NaN | 0.32247 |
| 3 | 782049285 | 234312603 | 47180.82 | -0.58054 | -0.00045401 | -0.46054 |
| 2 | 117257029 | 234312603 | 38721.94 | -0.93501 | -0.0010964 | -0.19664 |
| 3 | 782049285 | 234312603 | NaN | NaN | NaN | -0.60707 |
| 3 | 782049285 | 234312603 | 47256.8 | -0.42933 | -0.00033576 | -0.70423 |
| 3 | 782049285 | 234312603 | 47104.99 | -0.85091 | -0.00066545 | -0.34612 |
| 3 | 782049285 | 234312603 | 46783.95 | -0.96112 | -0.00075164 | -0.95532 |
| 3 | 782049285 | 234312603 | 47026.67 | -0.66347 | -0.00051887 | -0.428 |
| 3 | 78237729 | 234411004 | NaN | NaN | NaN | 0.13328 |
| 2 | 683360517 | 136470648 | NaN | NaN | NaN | NaN |
| 2 | 110601649 | 221001843 | 40031.52 | -0.93809 | -0.0010375 | 0.17847 |
| 2 | 110601649 | 221001843 | 39980.95 | -0.7294 | -0.00080672 | 0.064339 |
| 2 | 110601649 | 221001843 | NaN | NaN | NaN | 0.45069 |
| 2 | 110601649 | 221001843 | 40122.95 | -0.48689 | -0.00053851 | 0.11751 |
| 2 | 110601649 | 221001843 | 39421.7 | -0.60565 | -0.00066986 | 0.046545 |
| 2 | 110601649 | 221001843 | 39367.34 | 0 | 0 | -0.48324 |
| 2 | 114599966 | 228998476 | 40352.94 | -0.60563 | -0.00069406 | 0.03998 |
| 3 | 764335531 | 228998476 | 48247.85 | -0.60554 | -0.00046284 | -0.14232 |
| 4 | 942699453 | 376676871 | NaN | NaN | NaN | 0.7398 |
| 4 | 942699453 | 376676871 | NaN | NaN | NaN | 0.44133 |
| 4 | 942699453 | 376676871 | NaN | NaN | NaN | 0.57015 |
| 4 | 942699453 | 376676871 | NaN | NaN | NaN | 0.62828 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 4 | 942699453 | 376676871 | 43554.6 | -0.24396 | -0.00022998 | -11793 |
| 3 | 812069803 | 243318758 | 47351.67 | -0.33769 | -0.00027423 | 0.75759 |
| 2 | 954971699 | 190792885 | 42136.86 | 0.16333 | 0.00015598 | -12736 |
| 2 | 954971699 | 190792885 | 42136.86 | 0.16333 | 0.00015598 | -12736 |
| 2 | 954971699 | 190792885 | 43141.78 | -0.34128 | -0.00032592 | -0.27091 |
| 2 | 862367787 | 172272102 | 45493.23 | -15807 | -0.0013632 | -0.2871 |
| 2 | 543273182 | 108453181 | NaN | NaN | NaN | NaN |
| 2 | 543273182 | 108453181 | NaN | NaN | NaN | NaN |
| 2 | 948917758 | 189582096 | NaN | NaN | NaN | NaN |
| 2 | 948917758 | 189582096 | NaN | NaN | NaN | NaN |
| 2 | 948917758 | 189582096 | NaN | NaN | NaN | NaN |
| 2 | 84133509 | 168065563 | 45027.15 | -0.89245 | -0.00075085 | 0.41865 |
| 2 | 84133509 | 168065563 | 44767.33 | -0.58062 | -0.0004885 | -0.38377 |
| 2 | 84133509 | 168065563 | 44982.43 | -0.63029 | -0.00053029 | 0.24525 |
| 2 | 84133509 | 168065563 | 45711.25 | 0 | 0 | -11744 |
| 2 | 84133509 | 168065563 | NaN | NaN | NaN | 0.69875 |
| 2 | 84133509 | 168065563 | NaN | NaN | NaN | -0.11447 |
| 2 | 84133509 | 168065563 | 43560.81 | -0.47621 | -0.00040065 | -0.33956 |
| 2 | 84133509 | 168065563 | 45250.93 | -0.87036 | -0.00073227 | -0.046635 |
| 2 | 84133509 | 168065563 | 45688.7 | -0.94427 | -0.00079445 | -0.28334 |
| 2 | 84133509 | 168065563 | 46313.07 | -0.57953 | -0.00048758 | -0.35958 |
| 2 | 84133509 | 168065563 | 45818.69 | -0.70187 | -0.0005905 | -0.055655 |
| 2 | 84133509 | 168065563 | 46058.67 | -0.88319 | -0.00074306 | 0.088149 |
| 2 | 622765061 | 124351557 | 49666.66 | -11675 | -0.00072709 | 0.72062 |
| 2 | 622765061 | 124351557 | 53750.39 | 0 | 0 | -0.36105 |
| 2 | 622765061 | 124351557 | 53765.87 | -0.68807 | -0.00042851 | -0.096821 |
| 2 | 622765061 | 124351557 | 49223.58 | -0.70701 | -0.0004403 | 0.21521 |
| 2 | 622765061 | 124351557 | 53622.12 | 0 | 0 | -0.33432 |
| 2 | 622765061 | 124351557 | 52022.43 | -0.23251 | -0.0001448 | -0.28415 |
| 2 | 622765061 | 124351557 | 53283.96 | -0.8521 | -0.00053066 | -0.026131 |
| 2 | 622765061 | 124351557 | 54265.55 | -0.51174 | -0.0003187 | 0.47838 |
| 2 | 622765061 | 124351557 | 49801.67 | -0.35894 | -0.00022353 | 0.1143 |
| 2 | 622765061 | 124351557 | 53179.15 | -0.50061 | -0.00031176 | 0.29178 |
| 2 | 622765061 | 124351557 | 54084.26 | -0.31982 | -0.00019917 | -0.43446 |
| 3 | 72669461 | 2177062 | NaN | NaN | NaN | NaN |
| 3 | 812032628 | 243307605 | NaN | NaN | NaN | -11897 |
| 2 | 651301613 | 130058867 | 48959.03 | -0.26603 | -0.00017327 | 11725 |
| 2 | 651301613 | 130058867 | 50046.32 | -0.73326 | -0.00047757 | 14704 |
| 2 | 619254852 | 123649515 | 53106.32 | -0.21324 | -0.00013205 | 13032 |
| 2 | 619254852 | 123649515 | 51842.47 | -0.24336 | -0.0001507 | 15959 |
| 2 | 671344678 | 13406748 | NaN | NaN | NaN | NaN |
| 3 | 768697134 | 230306957 | NaN | NaN | NaN | 10683 |
| 3 | 821683108 | 246202749 | NaN | NaN | NaN | 0.72795 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 3 | 821683108 | 246202749 | 46390.55 | -0.52842 | -0.00043419 | 0.18359 | |
| 3 | 821683108 | 246202749 | 46712.96 | -0.49176 | -0.00040407 | -0.048026 | |
| 3 | 821683108 | 246202749 | 46631.54 | -0.5666 | -0.00046556 | 0.12942 | |
| 3 | 821683108 | 246202749 | 46837.07 | -0.46708 | -0.00038379 | -0.087081 | |
| 3 | 821683108 | 246202749 | 46733.58 | -0.54819 | -0.00045044 | -0.36846 | |
| 2 | 905411329 | 180880811 | NaN | NaN | NaN | 0.84056 | |
| 4 | 385940632 | 153973342 | 66420.11 | 0.018018 | 0.069539 | -13849 | |
| 4 | 385940632 | 153973342 | 66350.92 | -0.27129 | -0.0001047 | -13766 | |
| 2 | 926902094 | 185178963 | 44362.79 | -0.85174 | -0.00078948 | -23454 | |
| 3 | 9094124 | 272521537 | NaN | NaN | NaN | 0.53441 | |
| 3 | 9094124 | 272521537 | NaN | NaN | NaN | 0.7078 | |
| 3 | 9094124 | 272521537 | 44209.95 | -0.57909 | -0.00052663 | 0.11881 | |
| 3 | 74103403 | 222008026 | NaN | NaN | NaN | -0.96098 | |
| 3 | 676307141 | 202589959 | NaN | NaN | NaN | 13318 | |
| 3 | 788043977 | 23611101 | 47177.56 | 0 | 0 | -0.95449 | |
| 3 | 105211134 | 315331218 | NaN | NaN | NaN | 0.088838 | |
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| 2 | 102896974 | 205592493 | 41073.05 | -0.52115 | -0.00053625 | 0.11019 | |
| 2 | 102896974 | 205592493 | 42349.81 | -0.25346 | -0.0002608 | -0.58571 | |
| 2 | 102896974 | 205592493 | 41294.95 | -0.6056 | -0.00062315 | -0.12905 | |
| 2 | 102896974 | 205592493 | 41438.02 | 0 | 0 | -0.67687 | |
| 3 | 686315585 | 205592493 | NaN | NaN | NaN | NaN | |
| 2 | 102896974 | 205592493 | 41382.49 | 0 | 0 | -0.21612 | |
| 2 | 102896974 | 205592493 | 40875.37 | -0.67242 | -0.0006919 | -0.46279 | |
| 3 | 671690264 | 201204896 | 51096.34 | -0.04967 | -0.33363 | -18587 | |
| 3 | 693327825 | 207696165 | NaN | NaN | NaN | 0.95663 | |
| 2 | 10394881 | 207696165 | NaN | NaN | NaN | 0.78001 | |
| 3 | 693327825 | 207696165 | 51124.58 | -0.24826 | -0.00017213 | -0.90324 | |
| 2 | 728702169 | 145538978 | NaN | NaN | NaN | NaN | |
| 3 | 700653767 | 209893947 | NaN | NaN | NaN | -0.27695 | |
| 2 | 962961855 | 192390916 | 42497.58 | -1186 | -0.0011421 | -0.19763 | |
| 2 | 962961855 | 192390916 | NaN | NaN | NaN | -0.18423 | |
| 2 | 84536639 | 168871823 | 46651.53 | -0.60604 | -0.00051233 | 0.0019643 | |
| 2 | 84536639 | 168871823 | 46361.82 | 0 | 0 | -0.24501 | |
| 3 | 785376455 | 235310754 | 47188.41 | -0.56286 | -0.00044205 | -0.18373 | |
| 3 | 790708094 | 236910245 | 46846.98 | -0.63925 | -0.00050546 | -13783 | |
| 3 | 790708094 | 236910245 | 46786.05 | -0.61018 | -0.00048247 | -0.9336 | |
| 2 | 844389487 | 168676442 | NaN | NaN | NaN | -11825 | |
| 2 | 651312178 | 13006098 | NaN | NaN | NaN | NaN | |
| 2 | 608315912 | 121461727 | 53822.03 | -0.50827 | -0.00030919 | -15834 | |
| 2 | 826402579 | 16507906 | NaN | NaN | NaN | 19666 | |
| 2 | 826402579 | 16507906 | 44413.07 | -0.71751 | -0.00059296 | -0.17386 | |
| 2 | 826402579 | 16507906 | NaN | NaN | NaN | 20438 | |
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| | | | | | | |
|---|---|---|---|---|---|---|
| 2 | 826402579 | 16507906 | 45362.56 | -0.6055 | -0.00050038 | 0.23264 |
| 2 | 866385744 | 173075693 | 46475.25 | -0.60516 | -0.0005243 | 0.48461 |
| 2 | 891894799 | 178177504 | NaN | NaN | NaN | NaN |
| 2 | 667353026 | 13326915 | NaN | NaN | NaN | NaN |
| 2 | 755736567 | 150945858 | NaN | NaN | NaN | NaN |
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| 3 | 875689928 | 262404795 | 46945.66 | 0 | 0 | -0.25452 |
| 2 | 799900538 | 159778652 | 45334.03 | 0 | 0 | -14209 |
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| 2 | 799900538 | 159778652 | 47238.11 | -0.60566 | -0.00048447 | 0.065684 |
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| 3 | 988155981 | 296144611 | NaN | NaN | NaN | -0.4279 |
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| 3 | 696003393 | 208498835 | NaN | NaN | NaN | NaN |
| 3 | 86144196 | 258130405 | 45295.8 | -0.52496 | -0.00045222 | 0.18813 |
| 3 | 106950427 | 320549098 | 40548.52 | -0.22543 | -0.0002411 | -0.015594 |
| 2 | 717842491 | 143367043 | NaN | NaN | NaN | -12811 |
| 2 | 926900409 | 185178626 | 42856.25 | -10051 | -0.00093167 | -0.69765 |
| 2 | 739356789 | 147669903 | NaN | NaN | NaN | 0.43958 |
| 3 | 440230399 | 131766937 | 62752.88 | -0.20477 | -0.90147 | -0.60419 |
| 3 | 440230399 | 131766937 | 62672.29 | -0.27832 | -0.00012253 | 0.42741 |
| 3 | 982802767 | 294538647 | NaN | NaN | NaN | 14222 |
| 2 | 65182631 | 130163807 | 53177.34 | -0.078739 | -0.51324 | 13658 |
| 3 | 100810317 | 302128768 | NaN | NaN | NaN | 0.81854 |
| 3 | 100810317 | 302128768 | 41498.1 | -0.1923 | -0.00019385 | -0.69867 |
| 3 | 100810317 | 302128768 | 41709.66 | -0.69225 | -0.00069786 | -0.24163 |
| 4 | 954455923 | 381379459 | NaN | NaN | NaN | -0.43112 |
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| 4 | 954455923 | 381379459 | NaN | NaN | NaN | 0.73047 |
| 3 | 58895203 | 176383426 | NaN | NaN | NaN | 0.42039 |
| 3 | 627975057 | 188090334 | 52572.27 | -0.7764 | -0.00048756 | 0.44512 |
| 3 | 627975057 | 188090334 | 53267.84 | -0.11549 | -0.72523 | -0.59607 |
| 3 | 67168786 | 201204175 | 51096.34 | -0.04967 | -0.33363 | 17197 |
| 3 | 67168786 | 201204175 | 50391.08 | 0.0094576 | 0.063526 | 19131 |
| 3 | 67168786 | 201204175 | 47925.68 | 0.24981 | 0.0001678 | 13833 |
| 1 | 903418304 | 902411027 | NaN | NaN | NaN | 32655 |
| 3 | 616635936 | 184688598 | 53442.93 | -0.70568 | -0.00043514 | -0.78204 |
| 3 | 765738599 | 229419397 | 47979.82 | -0.85582 | -0.00065534 | 0.29911 |
| 3 | 765738599 | 229419397 | 49532.86 | -0.70076 | -0.0005366 | 0.056787 |
| 2 | 623309961 | 124460537 | NaN | NaN | NaN | NaN |
| 2 | 767816139 | 153361773 | 47355.37 | -0.91422 | -0.00070196 | 0.32816 |
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| | | | | | | |
|---|---|---|---|---|---|---|
| 2 | 874372637 | 174673072 | 45399.33 | -0.94238 | -0.00082399 | 0.8373 |
| 4 | 64181992 | 256325057 | NaN | NaN | NaN | 0.80509 |
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| 2 | 671854536 | 134169452 | 51400.14 | -0.34084 | -0.00022899 | -0.88366 |
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| 2 | 705334302 | 140865405 | NaN | NaN | NaN | NaN |
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| 3 | 707352305 | 211903509 | 50088.56 | -0.81337 | -0.00057534 | 0.54251 |
| 2 | 821919262 | 164182397 | 46434.6 | -0.73217 | -0.00060178 | -11055 |
| 3 | 912426655 | 273425814 | NaN | NaN | NaN | 14577 |

| Mass Error [D | Uncalibrated | Uncalibrated | Max intensity | Max intensity | Retention tim | Retention len |
|---|---|---|---|---|---|---|
| -0.03119 | -0.67506 | -0.00051395 | 7.6168E+14 | 7.6468E+14 | 73595 | 0.60837 |
| 0.00011031 | NaN | NaN | NaN | NaN | 78863 | 0.81698 |
| 0.00066902 | NaN | NaN | NaN | NaN | 67212 | 0.58141 |
| 0.00016907 | NaN | NaN | NaN | NaN | 71066 | 10799 |
| 0.00066715 | NaN | NaN | NaN | NaN | 58525 | 0.57363 |
| 0.0006082 | NaN | NaN | NaN | NaN | 63039 | 0.88077 |
| 0.00038378 | NaN | NaN | NaN | NaN | 63152 | 0.58234 |
| 0.0002275 | NaN | NaN | NaN | NaN | 67438 | 0.67523 |
| -0.00076819 | -10011 | -0.00076819 | 7.6769E+14 | 7.7036E+14 | 70.19 | 0.49585 |
| 0.0012503 | NaN | NaN | NaN | NaN | 93.17 | 11154 |
| -0.00018593 | NaN | NaN | NaN | NaN | 78.78 | 0.98734 |
| -0.00030454 | -0.43728 | -0.0002259 | 5.1659E+14 | 5.196E+14 | 88265 | 0.5152 |
| -0.00053259 | -12064 | -0.0009342 | 7.7438E+14 | 7.7889E+14 | 88249 | 13346 |
| -0.00013134 | NaN | NaN | NaN | NaN | 75278 | 0.52748 |
| NaN | NaN | NaN | NaN | NaN | 73177 | 1 |
| NaN | NaN | NaN | NaN | NaN | 73417 | 1 |
| NaN | NaN | NaN | NaN | NaN | 89034 | 1 |
| -0.00017778 | -0.53768 | -0.00042049 | 7.8238E+14 | 7.8506E+14 | 103.41 | 0.57672 |
| -0.0006593 | -15044 | -0.0011765 | 7.8238E+14 | 7.8539E+13 | 100.42 | 0.85462 |
| -0.0002705 | -10055 | -0.00078632 | 7.8205E+14 | 7.8539E+14 | 97275 | 10631 |
| 0.00025218 | NaN | NaN | NaN | NaN | 102.37 | 19762 |
| -0.00036016 | -10411 | -0.00081417 | 7.8238E+13 | 7.8539E+14 | 97438 | 0.64938 |
| -0.00023058 | -11317 | -0.0013269 | 1.1731E+14 | 1.1781E+14 | 97415 | 0.58425 |
| -0.00047476 | NaN | NaN | NaN | NaN | 102.5 | 13302 |
| -0.00055074 | -11336 | -0.0008865 | 7.8238E+14 | 7.8505E+14 | 97.99 | 10517 |
| -0.00027068 | -1197 | -0.00093614 | 7.8238E+14 | 7.8539E+14 | 105.34 | 0.73146 |
| -0.00074711 | -19164 | -0.0014987 | 7.8238E+14 | 7.8572E+13 | 100.21 | 0.42425 |
| -0.00033472 | -10915 | -0.00085358 | 7.8238E+14 | 7.8539E+14 | 98.64 | 0.56222 |
| 0.00010427 | NaN | NaN | NaN | NaN | 98032 | 0.47295 |
| NaN | NaN | NaN | NaN | NaN | 83069 | 1 |
| 0.00019739 | -0.75963 | -0.00084016 | 1.1065E+14 | 1.1115E+14 | 116.29 | 0.62392 |
| 0.07116 | -0.66506 | -0.00073556 | 1.1065E+14 | 1.111E+14 | 119.5 | 0.31782 |
| 0.00049847 | NaN | NaN | NaN | NaN | 126.64 | 0.47802 |
| 0.00012997 | -0.36938 | -0.00040854 | 1.1065E+14 | 1.111E+14 | 136.54 | 0.56355 |
| 0.51479 | -0.55911 | -0.00061838 | 1.1065E+14 | 1.111E+14 | 116.89 | 0.64877 |
| -0.00053448 | -0.48324 | -0.00053448 | 1.1065E+14 | 1.111E+14 | 117.13 | 0.53051 |
| 0.45817 | -0.56565 | -0.00064824 | 1.1465E+14 | 1.151E+14 | 126.86 | 0.8235 |
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| 0.00069741 | NaN | NaN | NaN | NaN | 79829 | 0.67028 |
| 0.00041604 | NaN | NaN | NaN | NaN | 78767 | 0.8231 |
| 0.00053748 | NaN | NaN | NaN | NaN | 77134 | 0.60345 |
| 0.00059228 | NaN | NaN | NaN | NaN | 81341 | 14287 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| -0.0011118 | -14233 | -0.0013418 | 9.4295E+13 | 9.4746E+14 | 78.16 | | 10275 |
| 0.00061522 | 0.4199 | 0.00034099 | 8.1241E+14 | 8.1541E+14 | 127.2 | | 15163 |
| -0.0012163 | -11103 | -0.0010603 | 9.5547E+14 | 9.5998E+14 | | 97553 | 13201 |
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| NaN | NaN | NaN | NaN | NaN | 145.85 | | 1 |
| 0.00035223 | -0.47379 | -0.00039862 | 8.4134E+14 | 8.4584E+14 | | 81717 | 0.60141 |
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| 0.74163 | -0.79504 | -0.00066889 | 8.4184E+14 | 8.4684E+14 | | 81927 | 0.48901 |
| 0.00044878 | -0.44689 | -0.00027831 | 6.2277E+14 | 6.2677E+14 | | 76755 | 15688 |
| -0.00022485 | -0.36105 | -0.00022485 | 6.2277E+14 | 6.2677E+14 | | 76205 | 0.73231 |
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| 0.71185 | -0.24463 | -0.00015235 | 6.2277E+14 | 6.2677E+14 | | 76455 | 16749 |
| 0.00018171 | -0.20884 | -0.00013006 | 6.2277E+14 | 6.2677E+14 | | 78722 | 0.7103 |
| -0.00027057 | -0.75428 | -0.00046974 | 6.2277E+14 | 6.2727E+14 | | 87866 | 0.6384 |
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| -0.0009661 | NaN | NaN | NaN | NaN | 68.89 | 0.65425 | |
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| 0.00095766 | 0.73712 | 0.00048009 | 6.513E+13 | 6.5932E+14 | | 48669 | 0.51516 |
| 0.000807 | 10899 | 0.00067495 | 6.1926E+14 | 6.2376E+14 | | 94877 | 0.67711 |
| 0.00098824 | 13525 | 0.00083754 | 6.1926E+14 | 6.2376E+14 | | 94214 | 0.52608 |
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| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.00015085 | -0.34483 | -0.00028334 | 8.2202E+14 | 8.2502E+14 | 101.81 | 0.72246 | |
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| 0.00076105 | NaN | NaN | NaN | NaN | 92142 | 0.93179 | |
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| -0.00071212 | NaN | NaN | NaN | NaN | 112.8 | 27081 | |
| 0.00090068 | NaN | NaN | NaN | NaN | 82156 | 0.76271 | |
| -0.00075218 | -0.95449 | -0.00075218 | 7.8838E+14 | 7.9172E+14 | 74365 | 0.92761 | |
| 0.93468 | NaN | NaN | NaN | NaN | 88133 | 0.81361 | |
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| NaN | NaN | NaN | NaN | NaN | 99695 | 1 | |
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| 0.00050497 | 0.080209 | 0.50796 | 6.3329E+14 | 6.378E+14 | 73482 | 0.64719 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| -0.00070432 | -14202 | -0.0011206 | 7.8938E+14 | 7.9238E+14 | 101.55 | | 2301 |
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| NaN | NaN | NaN | NaN | NaN | 158.33 | | 1 |
| -0.0012828 | -15622 | -0.00142 | 9.0894E+14 | 9.1345E+14 | | 84287 | 23439 |
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| 0.00080481 | NaN | NaN | NaN | NaN | | 87788 | 0.47366 |
| NaN | NaN | NaN | NaN | NaN | | 83317 | 1 |
| -0.00031152 | -11038 | -0.001145 | 1.0374E+14 | 1.0424E+13 | 108.15 | | 0.59637 |
| 0.18808 | NaN | NaN | NaN | NaN | 108.99 | | 0.44384 |
| -0.68931 | -0.80363 | -0.00083366 | 1.0374E+14 | 1.0424E+14 | 108.84 | | 0.54576 |
| NaN | NaN | NaN | NaN | NaN | | 47106 | 1 |
| 0.00073559 | NaN | NaN | NaN | NaN | | 66421 | 0.63902 |
| -0.00023388 | -1416 | -0.0013722 | 9.6942E+14 | 9.7844E+14 | | 64623 | 0.91163 |
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| 0.00037158 | NaN | NaN | NaN | NaN | | 64588 | 0.61862 |
| 0.00051315 | NaN | NaN | NaN | NaN | | 56769 | 0.68841 |
| 0.00025281 | NaN | NaN | NaN | NaN | | 55167 | 0.62209 |
| NaN | NaN | NaN | NaN | NaN | | 94476 | 1 |
| NaN | NaN | NaN | NaN | NaN | 113.66 | | 1 |
| NaN | NaN | NaN | NaN | NaN | 101.06 | | 1 |
| -0.00012533 | -0.87695 | -0.00066937 | 7.6363E+14 | 7.693E+14 | | 87498 | 0.53297 |
| 0.00023921 | -0.26883 | -0.00019687 | 7.3232E+13 | 7.4067E+14 | | 87227 | 0.6408 |
| 0.00066237 | -0.1163 | -8.47E-05 | 7.2865E+14 | 7.3399E+14 | 61.07 | | 0.54445 |
| 0.0010234 | NaN | NaN | NaN | NaN | | 75437 | 0.8054 |
| 0.0010338 | 0.60982 | 0.00051646 | 8.4741E+14 | 8.5592E+14 | | 88247 | 0.58873 |
| -0.0010046 | NaN | NaN | NaN | NaN | 97.45 | | 0.86969 |
| 0.00077487 | NaN | NaN | NaN | NaN | | 85368 | 13406 |
| 0.00066917 | NaN | NaN | NaN | NaN | | 57495 | 0.41724 |
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| 0.012008 | -0.55212 | -0.00034928 | 6.3261E+14 | 6.3828E+14 | | 63476 | 0.71551 |
| 0.00036841 | NaN | NaN | NaN | NaN | 66.49 | | 0.72619 |
| 0.00040937 | NaN | NaN | NaN | NaN | | 57738 | 0.36544 |

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|---|---|---|---|---|---|---|---|
| -0.00032366 | -10283 | -0.00065052 | 6.3261E+14 | 6.3828E+14 | 55677 | 0.57108 | |
| 0.00025897 | -0.54539 | -0.00056389 | 1.0339E+14 | 1.0424E+13 | 98.44 | 0.51672 | |
| 0.00068639 | 0.48783 | 0.00036963 | 7.5771E+14 | 7.6339E+14 | 121.46 | 18293 | |
| -0.0013081 | NaN | NaN | NaN | NaN | 71685 | 20642 | |
| -0.00013544 | NaN | NaN | NaN | NaN | 45.23 | 0.52084 | |
| NaN | NaN | NaN | NaN | NaN | 71708 | 1 | |
| 0.00014577 | -0.16979 | -0.00012446 | 7.3335E+14 | 7.3902E+14 | 104.82 | 14964 | |
| 0.00044319 | NaN | NaN | NaN | NaN | 135.41 | 0.67035 | |
| -0.0016135 | -28261 | -0.0021961 | 7.774E+14 | 7.8307E+14 | 86374 | 10412 | |
| 0.0013983 | 13945 | 0.0012577 | 9.0193E+14 | 9.0644E+14 | 95482 | 11019 | |
| 0.00050554 | NaN | NaN | NaN | NaN | 121.3 | 0.4834 | |
| -0.22425 | NaN | NaN | NaN | NaN | 147.46 | 0.71451 | |
| NaN | NaN | NaN | NaN | NaN | 129.23 | 1 | |
| NaN | NaN | NaN | NaN | NaN | 49.11 | 1 | |
| 0.00019561 | NaN | NaN | NaN | NaN | 57966 | 0.90657 | |
| 0.00022854 | NaN | NaN | NaN | NaN | 92568 | 0.82124 | |
| 0.000564 | NaN | NaN | NaN | NaN | 95027 | 0.59917 | |
| NaN | NaN | NaN | NaN | NaN | 121.25 | 1 | |
| 0.00044116 | 0.21447 | 0.00012174 | 5.676E+14 | 5.7094E+14 | 93914 | 0.86501 | |
| 0.0010246 | NaN | NaN | NaN | NaN | 93985 | 0.59921 | |
| -0.37578 | -0.6466 | -0.00053725 | 8.3138E+14 | 8.3539E+14 | 104.81 | 0.75336 | |
| 0.0011531 | NaN | NaN | NaN | NaN | 124.65 | 27934 | |
| 0.00035354 | -0.6641 | -0.00049211 | 7.4102E+14 | 7.4469E+14 | 87759 | 0.98688 | |
| 0.0015127 | 0.96818 | 0.00083206 | 8.5941E+14 | 8.6392E+13 | 108.02 | 0.7541 | |
| 0.0019138 | 15587 | 0.0013395 | 8.5991E+14 | 8.6342E+14 | 106.82 | 0.74968 | |
| 0.00048727 | -0.10261 | -0.78022 | 7.6074E+14 | 7.6341E+14 | 125.55 | 11819 | |
| -0.00085709 | -0.74789 | -0.00062649 | 8.3801E+14 | 8.4101E+14 | 103.81 | 0.70619 | |
| -0.0011037 | NaN | NaN | NaN | NaN | 59949 | 0.91953 | |
| -0.00064366 | NaN | NaN | NaN | NaN | 59764 | 0.9465 | |
| -0.00092598 | NaN | NaN | NaN | NaN | 61765 | 1128 | |
| -0.0012451 | NaN | NaN | NaN | NaN | 123.93 | 0.76739 | |
| 0.00068932 | 0.42296 | 0.00026757 | 6.3261E+14 | 6.3862E+14 | 63899 | 0.77814 | |
| NaN | NaN | NaN | NaN | NaN | 92513 | 1 | |
| 0.027706 | -18612 | -0.0016926 | 9.0994E+14 | 9.1394E+14 | 88764 | 0.6004 | |
| -0.00072269 | -17281 | -0.0010483 | 6.0663E+14 | 6.0996E+14 | 89718 | 14088 | |
| -0.00077341 | -13769 | -0.00083528 | 6.0663E+14 | 6.0963E+14 | 89.86 | 11759 | |
| -0.0006508 | -14476 | -0.00087818 | 6.0663E+14 | 6.0963E+14 | 89509 | 0.76118 | |
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| -0.0015969 | -20596 | -0.0018453 | 8.9644E+14 | 9.0094E+14 | 74517 | 0.44894 | |
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| 0.00043523 | NaN | NaN | NaN | NaN | 86999 | 0.7193 | |
| 0.0011086 | NaN | NaN | NaN | NaN | 85962 | 0.63573 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0015461 | NaN | NaN | NaN | NaN | 84968 | 0.63683 | |
| 0.05531 | NaN | NaN | NaN | NaN | 82974 | 0.69716 | |
| 0.0012608 | NaN | NaN | NaN | NaN | 84321 | 0.64992 | |
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| -0.00047223 | NaN | NaN | NaN | NaN | 148.56 | 0.90619 | |
| 0.001186 | NaN | NaN | NaN | NaN | 96381 | 0.94798 | |
| -0.00142 | NaN | NaN | NaN | NaN | 90.9 | 0.50488 | |
| 0.00019157 | -0.085767 | -0.42687 | 4.9771E+14 | 5.0172E+14 | 84455 | 0.5863 | |
| -0.0012119 | NaN | NaN | NaN | NaN | 134.05 | 0.67351 | |
| 0.00055962 | NaN | NaN | NaN | NaN | 114.39 | 0.52245 | |
| 0.00096424 | 0.21912 | 0.00016453 | 7.5085E+13 | 7.5535E+14 | 90274 | 11238 | |
| -0.00033326 | NaN | NaN | NaN | NaN | 95998 | 0.73493 | |
| 0.00037473 | NaN | NaN | NaN | NaN | 105 | 0.64604 | |
| -0.00036333 | -10028 | -0.00091697 | 9.1474E+14 | 9.1841E+14 | 95819 | 0.87028 | |
| -0.00086817 | NaN | NaN | NaN | NaN | 76414 | 0.88351 | |
| -0.0011211 | NaN | NaN | NaN | NaN | 73243 | 10119 | |
| -0.00021767 | -10359 | -0.00057521 | 5.5527E+14 | 5.6095E+14 | 55913 | 0.41409 | |
| -0.00025435 | -12069 | -0.0010046 | 8.3241E+14 | 8.4142E+14 | 57181 | 0.44668 | |
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| 0.000444 | -0.16528 | -0.00013758 | 8.3241E+14 | 8.4092E+14 | 64475 | 0.49722 | |
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| -0.0007084 | -16961 | -0.0010142 | 5.9797E+14 | 6.0665E+14 | 46122 | 0.3931 | |
| -0.00079715 | -17929 | -0.0010721 | 5.9797E+14 | 6.0632E+14 | 52587 | 0.64492 | |
| -0.0010275 | -22387 | -0.001541 | 6.8833E+14 | 6.9283E+14 | 85365 | 14531 | |
| NaN | NaN | NaN | NaN | NaN | 72982 | 1 | |
| 0.000504 | NaN | NaN | NaN | NaN | 117.77 | 12158 | |
| NaN | NaN | NaN | NaN | NaN | 88941 | 1 | |
| -0.00071071 | NaN | NaN | NaN | NaN | 105.25 | 16989 | |
| -0.00099964 | NaN | NaN | NaN | NaN | 124.28 | 12887 | |
| 0.00014077 | 0.21302 | 0.00010287 | 4.8289E+14 | 4.859E+13 | 45681 | 0.70065 | |
| 0.00049587 | 0.68809 | 0.00033227 | 4.8289E+14 | 4.859E+14 | 45763 | 0.59803 | |
| 0.00044906 | -0.69823 | -0.00052669 | 7.5467E+13 | 7.6268E+14 | 71015 | 0.46674 | |
| 0.00033729 | -0.23648 | -0.00017839 | 7.5467E+14 | 7.6301E+14 | 69722 | 0.74473 | |
| 0.14529 | -0.67934 | -0.00051245 | 7.5467E+14 | 7.6268E+14 | 81242 | 0.67423 | |
| 0.00074417 | NaN | NaN | NaN | NaN | 115.73 | 0.92355 | |
| 0.00033928 | 0.17765 | 0.99176 | 5.5825E+14 | 5.6126E+14 | 46373 | 13627 | |
| 0.00058073 | NaN | NaN | NaN | NaN | 48931 | 0.67912 | |
| 0.00043965 | 0.24558 | 0.00022985 | 9.3596E+14 | 9.4097E+14 | 116.18 | 0.55276 | |
| 0.0013452 | 0.36076 | 0.00034578 | 9.5848E+14 | 9.6298E+13 | 130.53 | 1487 | |
| 0.00099024 | 0.89689 | 0.00085964 | 9.5898E+14 | 9.6349E+14 | 132 | 15108 | |
| 0.00092516 | NaN | NaN | NaN | NaN | 82967 | 0.77986 | |
| -0.00078979 | -20573 | -0.0012565 | 6.1074E+14 | 6.1475E+14 | 116.71 | 0.92902 | |

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|---|---|---|---|---|---|---|---|
| -0.00089042 | | -18703 | -0.0011423 | 6.1074E+13 | 6.1475E+14 | 46818 | 0.65672 |
| -0.00071657 | | -20239 | -0.0012199 | 6.0275E+14 | 6.0725E+14 | 126.59 | 17975 |
| 0.00083546 | | 23154 | 0.00098447 | 4.2519E+13 | 4.2786E+14 | 127.92 | 23453 |
| -0.00010582 | NaN | | NaN | NaN | NaN | 73446 | 0.85529 |
| -0.00034272 | NaN | | NaN | NaN | NaN | 71689 | 0.95847 |
| -0.00046481 | NaN | | NaN | NaN | NaN | 68475 | 0.57893 |
| -0.00013785 | NaN | | NaN | NaN | NaN | 63488 | 0.81966 |
| -0.0001687 | NaN | | NaN | NaN | NaN | 128.62 | 23097 |
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| -0.00070165 | NaN | | NaN | NaN | NaN | 118.8 | 25957 |
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| -0.00060946 | NaN | | NaN | NaN | NaN | 129.27 | 2961 |
| -0.0005495 | NaN | | NaN | NaN | NaN | 69.77 | 10571 |
| -0.00026694 | NaN | | NaN | NaN | NaN | 63333 | 0.77888 |
| 0.0010827 | NaN | | NaN | NaN | NaN | 114.04 | 0.57431 |
| 0.60072 | -0.74429 | | -0.00069328 | 9.3147E+14 | 9.3598E+14 | 113.71 | 0.57819 |
| 0.58046 | -0.41494 | | -0.00027553 | 6.6435E+14 | 6.7003E+13 | 100.49 | 0.50895 |
| 0.00020745 | -0.050695 | | -0.33663 | 6.6402E+14 | 6.6969E+14 | 101.5 | 0.65757 |
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| NaN | NaN | | NaN | NaN | NaN | 73341 | 1 |
| NaN | NaN | | NaN | NaN | NaN | 116.91 | 1 |
| 0.0010872 | NaN | | NaN | NaN | NaN | 76655 | 2995 |
| 0.0010091 | NaN | | NaN | NaN | NaN | 73568 | 31739 |
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| -0.0016654 | NaN | | NaN | NaN | NaN | 87.75 | 0.77527 |
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| -0.0010843 | | -25621 | -0.0023301 | 9.0994E+14 | 9.1394E+14 | 100.58 | 17367 |
| -0.00026826 | 0.35344 | | 0.00021941 | 6.2077E+14 | 6.2528E+14 | 119.83 | 12677 |
| 0.00076401 | NaN | | NaN | NaN | NaN | 54759 | 0.54944 |
| 0.00069075 | NaN | | NaN | NaN | NaN | 52031 | 0.43327 |
| -0.0004052 | | -13824 | -0.00099161 | 7.1763E+14 | 7.2097E+14 | 62327 | 11715 |
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| 0.00059057 | NaN | | NaN | NaN | NaN | 52195 | 0.50599 |
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|---|---|---|---|---|---|---|---|
| -0.00034486 | | -14158 | -0.0010155 | 7.1763E+14 | 7.2063E+14 | 52567 | 0.85705 |
| 0.00044003 | NaN | | NaN | NaN | NaN | 50.78 | 0.51909 |
| 0.0011183 | 0.98959 | | 0.00098016 | 9.9048E+14 | 9.9498E+14 | 130.2 | 14043 |
| 0.0016944 | 0.82589 | | 0.00081803 | 9.9048E+14 | 9.9548E+14 | 101.65 | 2687 |
| 0.0014991 | 0.79621 | | 0.00078863 | 9.9098E+14 | 9.9548E+14 | 102.56 | 18499 |
| 0.0010097 | 0.22998 | | 0.00022779 | 9.9048E+14 | 9.9548E+14 | 102.36 | 0.76945 |
| 0.0015818 | 0.81593 | | 0.00080816 | 9.9048E+14 | 9.9548E+14 | 102.16 | 0.55981 |
| -0.0010935 | | -19366 | -0.0017109 | 8.8378E+14 | 8.8678E+14 | 133.99 | 17068 |
| -0.0010714 | | -19323 | -0.0013745 | 7.1134E+14 | 7.1584E+14 | 90056 | 0.66355 |
| -0.0015102 | | -24071 | -0.0017122 | 7.1134E+14 | 7.1584E+14 | 90591 | 10372 |
| 0.0010802 | NaN | | NaN | NaN | NaN | 81284 | 13858 |
| 0.0012056 | NaN | | NaN | NaN | NaN | 81377 | 16813 |
| 0.68876 | NaN | | NaN | NaN | NaN | 81158 | 0.85651 |
| 0.00030001 | NaN | | NaN | NaN | NaN | 111.95 | 0.94267 |
| 0.00051464 | NaN | | NaN | NaN | NaN | 114.19 | 0.63842 |
| 0.00071529 | NaN | | NaN | NaN | NaN | 123.38 | 0.5867 |
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| -0.001608 | | -33195 | -0.0022251 | 6.703E+14 | 6.7331E+14 | 66.67 | 0.38632 |
| -0.0014848 | | -30196 | -0.0020241 | 6.703E+13 | 6.7331E+14 | 64794 | 0.56033 |
| NaN | NaN | | NaN | NaN | NaN | 41 | 1 |
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| 0.00049439 | NaN | | NaN | NaN | NaN | 42096 | 0.57529 |
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| 0.00055042 | NaN | | NaN | NaN | NaN | 42336 | 0.93044 |
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| 0.00015941 | NaN | | NaN | NaN | NaN | 57517 | 0.85898 |
| 0.00049395 | NaN | | NaN | NaN | NaN | 55509 | 0.62685 |
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| -0.00043785 | | -13261 | -0.00097824 | 7.3767E+14 | 7.4401E+14 | 53482 | 0.68179 |
| 0.46504 | NaN | | NaN | NaN | NaN | 106.88 | 10294 |
| -0.00050752 | | -13644 | -0.0010065 | 7.3767E+14 | 7.4367E+14 | 52.9 | 0.56873 |
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| -0.0018201 | | -17689 | -0.0018201 | 1.0295E+14 | 1.034E+14 | 119.81 | 11799 |
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|---|---|---|---|---|---|---|
| 0.00041865 | NaN | NaN | NaN | NaN | 120.4 | 0.50204 |
| -0.0018155 | -17644 | -0.0018155 | 1.029E+14 | 1.0335E+14 | 120.97 | 0.6772 |
| -0.0016632 | -16164 | -0.0016632 | 1.0295E+14 | 1.034E+14 | 121.12 | 13278 |
| -0.0011612 | -11285 | -0.0011612 | 1.0295E+13 | 1.034E+14 | 121.39 | 0.68147 |
| -0.0012866 | -14072 | -0.001448 | 1.0295E+14 | 1.034E+14 | 133.17 | 0.95207 |
| 0.0006433 | NaN | NaN | NaN | NaN | 133.21 | 0.64886 |
| -0.00041792 | -11295 | -0.0011622 | 1.029E+14 | 1.034E+14 | 133.07 | 1098 |
| -0.00049955 | -0.91365 | -0.00062705 | 6.8632E+14 | 6.8965E+14 | 133.09 | 0.57579 |
| 0.00012673 | NaN | NaN | NaN | NaN | 121.19 | 0.82292 |
| -0.00061214 | -14789 | -0.0015217 | 1.029E+14 | 1.0335E+13 | 121.83 | 0.82023 |
| 0.42672 | -0.82083 | -0.00056335 | 6.8665E+14 | 6.8965E+14 | 121.79 | 0.83508 |
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| 0.25233 | NaN | NaN | NaN | NaN | 121.87 | 0.56217 |
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| -0.00058993 | -0.69372 | -0.00071382 | 1.029E+14 | 1.0335E+14 | 123.85 | 24877 |
| 0.00011339 | -0.41096 | -0.00042286 | 1.029E+14 | 1.0335E+14 | 121.54 | 0.76222 |
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| -0.00069648 | -0.67687 | -0.00069648 | 1.0295E+14 | 1.034E+14 | 122.16 | 0.78681 |
| NaN | NaN | NaN | NaN | NaN | 122.13 | 1 |
| -0.00022238 | -0.21612 | -0.00022238 | 1.0295E+14 | 1.0335E+14 | 122.46 | 0.56194 |
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| -0.0012485 | -19084 | -0.0012818 | 6.7202E+14 | 6.7503E+14 | 136.58 | 0.83658 |
| 0.00066326 | NaN | NaN | NaN | NaN | 82514 | 0.82999 |
| 0.00081082 | NaN | NaN | NaN | NaN | 83068 | 0.49942 |
| -0.00062624 | -11515 | -0.00079837 | 6.9366E+14 | 6.97E+14 | 84379 | 0.89329 |
| NaN | NaN | NaN | NaN | NaN | 155.72 | 1 |
| -0.00019404 | NaN | NaN | NaN | NaN | 89253 | 0.60728 |
| -0.00019031 | -13837 | -0.0013324 | 9.6346E+14 | 9.6797E+14 | 104.82 | 0.48682 |
| -0.00017741 | NaN | NaN | NaN | NaN | 103.7 | 0.42697 |
| 0.016606 | -0.60408 | -0.00051067 | 8.4537E+14 | 8.4987E+14 | 103.23 | 0.55985 |
| -0.00020713 | -0.24501 | -0.00020713 | 8.4537E+13 | 8.4937E+14 | 103.35 | 0.45023 |
| -0.0001443 | -0.74659 | -0.00058635 | 7.8571E+14 | 7.9139E+14 | 109.22 | 40656 |
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| NaN | NaN | NaN | NaN | NaN | 75723 | 1 |
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| 0.0016252 | NaN | NaN | NaN | NaN | 105.61 | 0.69661 |
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| 0.001689 | NaN | NaN | NaN | NaN | 105.18 | 0.58349 |
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|---|---|---|---|---|---|---|---|
| 0.00019225 | -0.37286 | -0.00030813 | 8.264E+14 | 8.3091E+14 | 99569 | 0.63045 | |
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| NaN | NaN | NaN | NaN | NaN | 121.67 | | 1 |
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| -0.00042284 | NaN | NaN | NaN | NaN | 109.96 | 0.50768 | |
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| -0.16677 | -0.24102 | -0.00025778 | 1.0702E+14 | 1.0732E+14 | 94485 | 0.76564 | |
| -0.00091965 | NaN | NaN | NaN | NaN | 51407 | 0.58632 | |
| -0.00064665 | -17028 | -0.0015783 | 9.269E+14 | 9.3191E+14 | 99424 | 0.74223 | |
| 0.00032501 | NaN | NaN | NaN | NaN | 128.19 | 0.34515 | |
| -0.00026598 | -0.80896 | -0.00035613 | 4.4023E+14 | 4.4858E+14 | 18285 | 0.77988 | |
| 0.00018816 | 0.14909 | 0.65632 | 4.4023E+14 | 4.4824E+14 | 23095 | 0.53612 | |
| 0.0013978 | NaN | NaN | NaN | NaN | 102.31 | 11992 | |
| 0.00089024 | 1287 | 0.00083892 | 6.5183E+14 | 6.6084E+14 | 75395 | 0.5929 | |
| 0.00082517 | NaN | NaN | NaN | NaN | 100.73 | 0.78802 | |
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| 0.00024759 | NaN | NaN | NaN | NaN | 50314 | 0.50629 | |
| 0.00027953 | -0.33127 | -0.00020803 | 6.2798E+14 | 6.3098E+14 | 65335 | 0.6929 | |
| -0.00037432 | -0.71156 | -0.00044684 | 6.2831E+14 | 6.3098E+14 | 64578 | 0.70169 | |
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| 0.001285 | 19226 | 0.0012914 | 6.7202E+14 | 6.7469E+14 | 123.02 | 49787 | |
| 0.00092914 | 16331 | 0.0010969 | 6.7202E+14 | 6.7469E+14 | 130.28 | 13125 | |
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|---|---|---|---|---|---|---|---|
| 0.00073212 | -0.10507 | -0.91872 | 8.7437E+14 | 8.7938E+14 | 74512 | 0.9054 | |
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| 0.00133 | NaN | NaN | NaN | NaN | 86106 | 16299 | |

| Calibrated re | Calibrated re | Calibrated re | Retention tim | Match time d | Match m/z di | Match q-valu |
|---|---|---|---|---|---|---|
| 88682 | 88396 | 89005 | 15086 | | | |
| 86296 | 85.84 | 86657 | 7433 | | | |
| 82298 | 82.03 | 82611 | 15086 | | | |
| 78199 | 77715 | 78795 | 71326 | | | |
| 73611 | 73316 | 73.89 | 15086 | | | |
| 70516 | 70158 | 71039 | 74774 | | | |
| 78238 | 78026 | 78608 | 15086 | | | |
| 74.77 | 74446 | 75121 | 73329 | | | |
| 77147 | 76906 | 77402 | 69571 | | | |
| 101.1 | 100.56 | 101.67 | 7932 | | | |
| 87514 | 86958 | 87945 | 87342 | | | |
| 93396 | 93101 | 93616 | 51308 | | | |
| 93.38 | 92952 | 94286 | 51308 | | | |
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| 89428 | 88928 | 89928 | 16251 | | | |
| 89.57 | 89.07 | 90.07 | 16153 | | | |
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| 104.38 | 104.12 | 104.7 | 0.96355 | | | |
| 104.58 | 104.14 | 104.99 | 4162 | | | |
| 104.8 | 104.24 | 105.3 | 75276 | | | |
| 103.74 | 103.3 | 105.28 | 13625 | | | |
| 104.52 | 104.19 | 104.84 | 7082 | | | |
| 104.53 | 104.22 | 104.81 | 71179 | | | |
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| 135.39 | 135.12 | 135.75 | 19095 | | | |
| 132.19 | 132.02 | 132.34 | 12687 | | | |
| 134.08 | 133.79 | 134.27 | 74366 | | | |
| 128.76 | 128.37 | 128.94 | -7775 | | | |
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| 84867 | 84016 | 85445 | 35258 | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 86894 | 86285 | 87312 | 87342 | | | |
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| 106.59 | 105.91 | 107.23 | 90348 | | | | |
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| 106.27 | 105.98 | 106.44 | 85719 | -0.158 | 0.0012713 | NaN | |
| | 57524 | 57252 | 57966 | 40333 | | | |
| | 84797 | 84297 | 85297 | 16253 | | | |
| 126.94 | 126.44 | 127.44 | 8889 | | | | |
| 154.65 | 154.15 | 155.15 | 51221 | | | | |
| 157.07 | 156.57 | 157.57 | 51221 | | | | |
| 154.53 | 154.03 | 155.03 | 86792 | | | | |
| 100.91 | 100.66 | 101.26 | 19196 | | | | |
| | 90685 | 90438 | 90985 | 5224 | | | |
| | 91882 | 91522 | 92181 | 71776 | | | |
| | 95804 | 95551 | 96123 | 13888 | | | |
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| 101.56 | 101.28 | 101.91 | 68355 | | | | |
| | 97518 | 97303 | 97853 | 15387 | | | |
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| | 83294 | 82811 | 84379 | 65389 | | | |
| | 74634 | 74321 | 75054 | -15717 | | | |
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| 93.44 | | 93001 | 94676 | 16985 | | | |
| 104.69 | 104.38 | 105.09 | 25969 | | | | |
| | 96344 | 96047 | 96686 | 84784 | 0.066776 | -0.00027052 | NaN |
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| | 60977 | 60734 | 61249 | 12307 | 0.11647 | 0.00019938 | NaN |
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| 101.92 | 101.66 | 102.42 | -10905 | | | | |

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| 102.87 | 102.55 | 103.27 | | 10635 |
| 106.32 | 105.95 | 106.71 | | 63039 |
| 106.6 | 106.18 | 107.26 | | -43689 |
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| 103.68 | 103.4 | 104.34 | | 11542 |
| | 58484 | 58195 | 58792 | 74781 |
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| | 89573 | 89404 | 89773 | 11064 |
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| 124.64 | 123.39 | 126.1 | | 11842 |
| 101.95 | 101.55 | 102.31 | 19.79 | |
| | 81322 | 80834 | 81762 | 69571 |
| | 93264 | 92876 | 93689 | 51308 |
| | 93584 | 93163 | 93855 | 49337 |
| | 93358 | 92951 | 93838 | 45084 |
| 107.15 | 106.65 | 107.65 | | 7456 |
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| 101.54 | 101.12 | 102.31 | | 62037 |
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| 84.35 | | 84065 | 84594 | 13861 |
| | 86597 | 86306 | 86935 | 15052 |
| | 87258 | 86975 | 87622 | 16.64 |
| 145.58 | 145.08 | 146.08 | | 0 |
| 113.25 | 112.75 | 113.75 | | -19476 |
| | 62278 | 61778 | 62778 | 15508 |
| | 84221 | 84021 | 84733 | 16078 |
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| 91.87 | | 91535 | 92183 | -20978 |
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| 81.54 | | 81279 | 81926 | 80581 |

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|---|---|---|---|---|---|---|---|
| | 92245 | 90874 | 93175 | -9306 | | | |
| | 93476 | 92567 | 96476 | -97767 | | | |
| 170.95 | 170.45 | 171.45 | | 22981 | | | |
| 104.55 | 103.89 | 106.23 | 20.26 | | | | |
| 105.39 | 104.22 | 107.37 | | 18419 | | | |
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| 105.36 | 105.17 | 105.64 | | 17569 | | | |
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| 127.03 | 126.78 | 127.37 | | 18882 | | | |
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| 127.99 | 127.68 | 128.23 | | 19151 | | | |
| | 58584 | 58084 | 59084 | 11478 | | | |
| | 78645 | 78.34 | 78979 | 12223 | | | |
| | 79931 | 79545 | 80457 | 15308 | | | |
| | 79961 | 79545 | 80457 | 15308 | | | |
| | 80397 | 80116 | 80734 | 15809 | | | |
| 70.53 | | 70261 | 70949 | 13761 | | | |
| | 70475 | 70141 | 70763 | 15308 | | | |
| 104.01 | 103.51 | 104.51 | | 95334 | | | |
| | 91039 | 90539 | 91539 | -22.62 | | | |
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| | 93917 | 93654 | 94187 | 64188 | | | |
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| | 64196 | 63923 | 64467 | 3126 | | | |
| | 89889 | 89408 | 90214 | 14452 | | | |
| | 93378 | 93101 | 93689 | 51308 | | | |
| 103.85 | 103.54 | 104.41 | | 64039 | | | |
| 103.99 | 103.58 | 104.92 | | 18619 | | | |
| | 64873 | 64649 | 65066 | 73776 | | | |
| | 70036 | 69.74 | 70298 | 16277 | | | |
| 71.41 | | 70984 | 71.7 | 79337 | | | |
| | 67525 | 67.14 | 67866 | 10349 | | | |
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|---|---|---|---|---|---|---|---|
| | 67784 | 67514 | 68086 | 12107 | | | |
| 105.98 | 105.76 | 106.28 | | 75362 | | | |
| 133.3 | 132.42 | 134.24 | | 11842 | | | |
| | 88325 | 87935 | 89999 | 16.64 | | | |
| | 52736 | 52515 | 53036 | 75058 | | | |
| | 87218 | 86718 | 87718 | 15.51 | | | |
| 106.08 | 105.4 | 106.89 | | 12623 | | | |
| 144.35 | 144.08 | 144.75 | | 89371 | | | |
| 104.74 | 104.39 | 105.43 | | 18364 | | | |
| 103.14 | 102.67 | 103.77 | | 76569 | | | |
| 129.74 | 129.5 | 129.98 | | 84358 | | | |
| 119.86 | 119.65 | 120.37 | | -27593 | | | |
| 143.58 | 143.08 | 144.08 | | 14347 | | | |
| | 65487 | 64987 | 65987 | 16377 | | | |
| | 66401 | 65792 | 66699 | 84343 | | | |
| | 94224 | 93828 | 94649 | 16565 | | | |
| 94.34 | | 93993 | 94592 | -0.68662 | | | |
| 133.1 | 132.6 | 133.6 | | 11854 | | | |
| 101.15 | 100.8 | 101.67 | | 45474 | | | |
| 101.22 | 100.93 | 101.53 | | 45474 | | | |
| | 93199 | 92837 | 93591 | -11611 | | | |
| 133.29 | 131.63 | 134.42 | | 86365 | | | |
| 105.33 | 104.94 | 105.93 | | 17569 | | | |
| 103.74 | 103.37 | 104.12 | | -42799 | | | |
| 103.83 | 103.45 | 104.2 | | -29879 | 0.042553 | 0.00035826 | NaN |
| 131.63 | 131.07 | 132.25 | | 60754 | | | |
| 105.93 | 105.64 | 106.35 | | 2122 | | | |
| | 74601 | 74277 | 75196 | 14652 | | | |
| 74.91 | | 74549 | 75496 | 15146 | | | |
| | 74532 | 74252 | 75.38 | | 12766 | | |
| 104.46 | 104.26 | 105.03 | | -19476 | | | |
| | 72377 | 71964 | 72742 | 84783 | | | |
| | 91123 | 90623 | 91623 | -13898 | | | |
| | 92904 | 92636 | 93236 | 41393 | | | |
| | 94746 | 94091 | 95.5 | | 50272 | | |
| | 94791 | 94313 | 95489 | 49305 | -0.041153 | -0.00017331 | NaN |
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| | 82757 | 81481 | 83455 | 14552 | | | |
| | 89364 | 89119 | 89568 | 14847 | | | |
| | 89433 | 89182 | 89851 | 14452 | 0.034115 | 0.00081033 | NaN |
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| 102.39 | 102.07 | 102.71 | | 16433 | | | |

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|---|---|---|---|---|---|---|
| 102.64 | 102.25 | 102.89 | 17669 | | | |
| 89947 | 89633 | 90.33 | 69729 | | | |
| 102.68 | 102.23 | 102.88 | 18364 | | | |
| 102.6 | 102.23 | 103.19 | 18858 | | | |
| 116.63 | 116.01 | 116.7 | -19476 | | | |
| 120.97 | 120.7 | 121.61 | -27593 | | | |
| 103 | 102.66 | 103.61 | 66148 | | | |
| 93285 | 93126 | 93.63 | 2385 | | | |
| 102.02 | 101.72 | 102.31 | 17569 | | | |
| 146.41 | 146.09 | 146.76 | 12352 | | | |
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| 94413 | 94085 | 95209 | 41393 | | | |
| 89819 | 89454 | 90189 | -61797 | | | |
| 106.31 | 106.07 | 106.72 | 1319 | | | |
| 102.66 | 102.21 | 103.08 | 68448 | | | |
| 90174 | 89.72 | 90604 | 13.76 | | | |
| 89782 | 89365 | 90377 | 16.54 | | | |
| 70999 | 70781 | 71195 | 15086 | | | |
| 69999 | 69.77 | 70217 | 12818 | | | |
| 66729 | 66453 | 66989 | 10349 | | | |
| 67301 | 67076 | 67574 | 28262 | | | |
| 66751 | 66453 | 66934 | 10349 | -0.27472 | -0.00060714 | NaN |
| 61208 | 61025 | 61419 | 15086 | | | |
| 60065 | 59868 | 60513 | 74781 | | | |
| 101.28 | 100.89 | 102.34 | 15915 | | | |
| 89233 | 88733 | 89733 | 16251 | | | |
| 132.72 | 132.38 | 133.59 | 14948 | | | |
| 93874 | 93374 | 94374 | 49336 | | | |
| 90902 | 90085 | 91784 | -14345 | | | |
| 138.83 | 138.39 | 139.68 | 14547 | | | |
| 55.76 | 55435 | 56135 | 10079 | | | |
| 55303 | 54953 | 55551 | 95401 | -0.22856 | 0.00039447 | NaN |
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| 82.54 | 82217 | 82961 | 12818 | | | |
| 83176 | 82873 | 83547 | 19343 | | | |
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| 61.82 | 61491 | 62854 | 15446 | | | |
| 64376 | 63856 | 64536 | 15445 | | | |
| 133.71 | 133.39 | 133.94 | 17524 | | | |
| 132.31 | 131.6 | 133.09 | 17792 | | | |
| 138.47 | 137.36 | 138.88 | 64748 | | | |
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111.63      110.84      113.18             -16286
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      79353       79035       79614       10877
      79841       79541       80361       16353
137.41      136.35      138.66             29068
      79605       79349       80152       11564
      79533 79.2                80362       13018
      79571       79233       80252       15146
117.36      115.3       119.21      -4.41
      78254       78052 78.59               71326
      78607       78338       79434       12349
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      79322       78967       80009       15308
117.33      115.93      118.52              -1474
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112.99      111.61      114.57             -16286
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      94015 93.77               94428      -74859 -0.24157      0.00018964   NaN
105.3       104.93      106.12              43696
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        133 132.5       133.5               16087
      90416       89521       92516 13.76
      90107       89054       92228 16.54
126.53      125.15      127.99             10477
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108.24      107.92      109.32             -16286
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      65937 65.78               66329       11178
      68308 68.1                68534       16277
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```

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| 140.47 | 139.46 | 141.16 | | 64747 | | | |
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| 130.72 | 130.46 | 131.1 | | 16528 | | | |
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| 59.31 | | 58947 | 59.67 | 16975 | | | |
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| | 58862 | 58414 | 59503 | 15253 | | | |
| | 58767 | 58553 | 58876 | 83342 | | | |
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| 134.77 | 134.35 | 135.43 | | 14277 | | | |

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| 116.08 | 115.68 | 118.17 | -7775 | | | |
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| 131.31 | 131.05 | 131.67 | 10506 | | | |
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| 130.95 | 130.45 | 131.45 | 17664 | | | |
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| 140.4 | 140.21 | 140.56 | 12213 | | | |
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| 128.26 | 127.84 | 128.64 | 17564 | | | |
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| | | | | | | |
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| | 89336 | 88894 | 89799 | 14824 | | |
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| Match score | Number of da | Number of sc | Number of is | PIF | Fraction of to | Base peak fra |
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|---|---|---|---|---|---|---|---|
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|---|---|---|---|---|---|
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| | | | | | | | |
|---|---|---|---|---|---|---|---|
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| | 382 | 50 | 12 | 0 | 0 | 0 | |
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| | 149 | 34 | 8 | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
| | 190 | 32 | 10 | 0 | 0 | 0 | |
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| | 114 | 13 | 13 | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
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| | 73 | 15 | 7 | 0 | 0 | 0 | |
| | 70 | 9 | 11 | 0 | 0 | 0 | |
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| | 32 | 7 | 7 | 0 | 0 | 0 | |
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| | | | | 0 | 0 | 0 | |
| | 120 | 28 | 7 | 0 | 0 | 0 | |
| | 88 | 33 | 6 | 0 | 0 | 0 | |
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|---|---|---|---|---|---|---|---|---|
| | | | | | | | | |
| | | | | | | | | |
| | | 208 | 31 | 10 | 0 | 0 | 0 | |
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| | | 90 | 24 | 6 | 0 | 0 | 0 | |
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| | | 121 | 20 | 14 | 0 | 0 | 0 | |
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| | | | | | 0 | 0 | 0 | |
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| | | | | | 0 | 0 | 0 | |
| | | 49 | 11 | 6 | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
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| | | 170 | 23 | 11 | 0 | 0 | 0 | |
| | 41621 | 115 | 15 | 10 | NaN | NaN | NaN | |
| | 41621 | 127 | 25 | 9 | NaN | NaN | NaN | |
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| 43.69 | | 49 | 8 | 10 | NaN | NaN | NaN | |
| | 44246 | 164 | 38 | 7 | NaN | NaN | NaN | |
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| | 28 | 8 | 5 | 0 | 0 | 0 |
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| | 90 | 20 | 8 | 0 | 0 | 0 |
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| | | | | 0 | 0 | 0 |
| | 488 | 58 | 12 | 0 | 0 | 0 |
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| | 138 | 25 | 8 | 0 | 0 | 0 |
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| | 184 | 26 | 12 | 0 | 0 | 0 |
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| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
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| | | | | 0 | 0 | 0 |
| | 497 | 80 | 15 | 0 | 0 | 0 |
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| | | | | | | |
|---|---|---|---|---|---|---|
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| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 45 | 9 | 7 | 0 | 0 | 0 |
| | 32 | 6 | 8 | 0 | 0 | 0 |
| 96777 | 29 | 8 | 6 | NaN | NaN | NaN |
| | 163 | 30 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 123 | 36 | 6 | 0 | 0 | 0 |
| | 197 | 83 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 67 | 16 | 11 | 0 | 0 | 0 |
| | 56 | 7 | 12 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 239 | 30 | 12 | 0 | 0 | 0 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | 346 | 40 | 12 | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 136 | 20 | 10 | 0 | 0 | 0 | |
| | | 301 | 34 | 14 | 0 | 0 | 0 | |
| | | 196 | 26 | 16 | 0 | 0 | 0 | |
| | 47622 | 217 | 25 | 13 | NaN | NaN | NaN | |
| | 47622 | 219 | 30 | 12 | NaN | NaN | NaN | |
| | | 234 | 24 | 13 | 0 | 0 | 0 | |
| | | 103 | 25 | 6 | 0 | 0 | 0 | |
| 64.82 | | 197 | 36 | 9 | NaN | NaN | NaN | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 66 | 11 | 10 | 0 | 0 | 0 | |
| | 43115 | 123 | 24 | 8 | NaN | NaN | NaN | |
| | 43115 | 45 | 8 | 9 | NaN | NaN | NaN | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 287 | 34 | 12 | 0 | 0 | 0 | |
| | | 161 | 32 | 8 | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 79 | 25 | 5 | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 41 | 7 | 10 | 0 | 0 | 0 | |
| | 40432 | 52 | 9 | 10 | NaN | NaN | NaN | |
| | | | | | 0 | 0 | 0 | |
| | | 86 | 10 | 13 | 0 | 0 | 0 | |
| | | 61 | 10 | 9 | 0 | 0 | 0 | |
| | | | | | 0 | 0 | 0 | |
| | | 235 | 30 | 12 | 0 | 0 | 0 | |
| | | 130 | 15 | 14 | 0 | 0 | 0 | |
| | | 752 | 79 | 15 | 0 | 0 | 0 | |
| | | 709 | 71 | 15 | 0 | 0 | 0 | |
| | | 190 | 39 | 8 | 0 | 0 | 0 | |
| | | 130 | 13 | 14 | 0 | 0 | 0 | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | 0 | 0 | 0 |
| | | 282 | 45 | 10 | | 0 | 0 | 0 |
| | | 865 | 89 | 14 | | 0 | 0 | 0 |
| | | 211 | 45 | 7 | | 0 | 0 | 0 |
| | | 135 | 15 | 13 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 109 | 15 | 13 | | 0 | 0 | 0 |
| | | 41 | 7 | 9 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 442 | 54 | 12 | | 0 | 0 | 0 |
| | | 170 | 55 | 6 | | 0 | 0 | 0 |
| | | 421 | 52 | 11 | | 0 | 0 | 0 |
| | | 428 | 50 | 11 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 834 | 147 | 10 | | 0 | 0 | 0 |
| | | 48 | 9 | 8 | | 0 | 0 | 0 |
| | | 214 | 42 | 8 | | 0 | 0 | 0 |
| | | 1043 | 126 | 15 | | 0 | 0 | 0 |
| | | 391 | 55 | 10 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 194 | 38 | 8 | | 0 | 0 | 0 |
| 128.33 | | 556 | 63 | 12 | NaN | NaN | NaN | |
| | | 93 | 12 | 15 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 342 | 59 | 9 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 45 | 9 | 8 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 203 | 37 | 8 | | 0 | 0 | 0 |
| | 86179 | 128 | 30 | 6 | NaN | NaN | NaN | |
| | | 513 | 53 | 15 | | 0 | 0 | 0 |
| | | 71 | 11 | 10 | | 0 | 0 | 0 |
| | 40177 | 93 | 22 | 7 | NaN | NaN | NaN | |
| | | | | | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 280 | 52 | 9 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 88 | 27 | 5 | | 0 | 0 | 0 |
| | | | | | | 0 | 0 | 0 |
| | | 81 | 21 | 7 | | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | |
| | | | | | | |
| | 154 | 42 | 7 | 0 | 0 | 0 |
| | 132 | 34 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 181 | 35 | 8 | 0 | 0 | 0 |
| | 172 | 31 | 9 | 0 | 0 | 0 |
| | 147 | 37 | 7 | 0 | 0 | 0 |
| | 152 | 30 | 7 | 0 | 0 | 0 |
| | 255 | 41 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 162 | 31 | 7 | 0 | 0 | 0 |
| | 278 | 26 | 17 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 131 | 18 | 11 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 258 | 50 | 7 | 0 | 0 | 0 |
| | 112 | 37 | 6 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 22 | 7 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 92 | 10 | 13 | 0 | 0 | 0 |
| | 76 | 10 | 11 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 191 | 27 | 10 | 0 | 0 | 0 |
| | 179 | 31 | 9 | 0 | 0 | 0 |
| | 93 | 12 | 15 | 0 | 0 | 0 |
| | 510 | 76 | 10 | 0 | 0 | 0 |
| | 72 | 17 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 559 | 75 | 10 | 0 | 0 | 0 |
| | 22 | 9 | 4 | 0 | 0 | 0 |
| 53551 | 26 | 9 | 6 | NaN | NaN | NaN |
| | | | | 0 | 0 | 0 |
| | 48 | 8 | 9 | 0 | 0 | 0 |
| | 65 | 12 | 8 | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 56 | 12 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 65 | 16 | 6 | 0 | 0 | 0 |
| 77288 | 81 | 22 | 6 | NaN | NaN | NaN |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 33 | 7 | 8 | 0 | 0 | 0 |
| | 25 | 7 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

| PEP | MS/MS Coun | MS/MS Scan | Score | | Delta score | Combinatoric | Ratio H/L |
|---|---|---|---|---|---|---|---|
| 0.0024998 | 1 | 8758 | | 50873 | 36926 | 10 | 0.32364 |
| 0.00066166 | 2 | 9811 | | 63937 | 45532 | 10 | 0.39827 |
| 0.011114 | 1 | 7485 | 56.48 | | 27381 | 5 | 0.189 |
| 0.015999 | 1 | 8380 | | 54047 | 32371 | 5 | 0.27281 |
| 0.013065 | 1 | 5937 | | 41615 | 26992 | 5 | 0.25025 |
| 0.0012876 | 1 | 6660 | | 53625 | 31949 | 5 | 0.14797 |
| 0.00037934 | 1 | 6747 | | 55302 | 26579 | 10 | 0.2281 |
| 0.0045661 | 1 | 7721 | | 42209 | 20086 | 10 | 0.37424 |
| 0.014163 | 1 | 4648 | | 48579 | 48579 | 5 | 0.31534 |
| 0.012897 | 1 | 13576 | | 48467 | 20106 | 3 | 65582 |
| 0.01963 | 1 | 9065 | | 80688 | 35.32 | 1 | NaN |
| 0.0063079 | 1 | 13327 | 73.36 | | 51447 | 1 | 0.3703 |
| 0.033103 | 1 | 13329 | | 80596 | 56065 | 1 | 0.58594 |
| 0.0053695 | 1 | 9268 | | 50827 | 18461 | 1 | NaN |
| 0.02807 | 1 | 10887 | | 45433 | 82528 | 1 | |
| 0.014498 | 1 | 7441 | | 57149 | 22.38 | 1 | |
| 0.027538 | 1 | 14169 | | 61344 | 22898 | 2 | |
| 0.0025375 | 3 | 15318 | | 67396 | 61087 | 2 | 0.54438 |
| 0.0010496 | 2 | 15421 | | 76533 | 55254 | 2 | 0.49769 |
| 0.98785 | 1 | 15234 | | 87352 | 62871 | 2 | 0.49671 |
| 0.0093801 | 1 | 17999 | 56.48 | | 28389 | 2 | 0.34323 |
| 0.0030875 | 1 | 15853 | | 58796 | 39861 | 2 | 0.49439 |
| 2.2007E-11 | 1 | 15878 | 118.67 | | 103.82 | 2 | 11087 |
| 0.011985 | 1 | 14078 | 54.15 | | 28274 | 2 | 0.16628 |
| 0.0013892 | 1 | 14879 | | 99409 | 80404 | 2 | 0.46245 |
| NaN | 0 | | NaN | | NaN | 0 | 0.55402 |
| NaN | 0 | | NaN | | NaN | 0 | 12755 |
| NaN | 0 | | NaN | | NaN | 0 | 0.57747 |
| 0.022911 | 1 | 16018 | | 47603 | 15.25 | 4 | 0.51852 |
| 0.0359 | 1 | 10643 | | 44612 | 89015 | 1 | |
| 0.0096279 | 1 | 16802 | 83.31 | | 83.31 | 5 | 0.62157 |
| 0.038931 | 1 | 18314 | | 65207 | 45627 | 5 | 0.53203 |
| 0.02059 | 1 | 20557 | | 96391 | 63022 | 5 | 0.43102 |
| 0.001369 | 1 | 12202 | | 95444 | 95444 | 5 | 0.63294 |
| 0.044014 | 1 | 8067 | | 63883 | 44861 | 5 | 0.59556 |
| NaN | 0 | | NaN | | NaN | 0 | 0.43797 |
| 0.0004661 | 2 | 8847 | 90.78 | | 72.2 | 10 | 0.51119 |
| 0.019791 | 1 | 8859 | | 43794 | 43794 | 10 | 0.47973 |
| 0.0023691 | 1 | 9284 | | 56099 | 33977 | 9 | 0.1246 |
| 0.0054448 | 1 | 10051 | | 51264 | 31511 | 9 | 0.081331 |
| 0.00031051 | 1 | 7891 | | 42301 | 20735 | 9 | 0.12181 |
| 0.00078287 | 1 | 10748 | | 40129 | 24923 | 9 | 0.18889 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.013428 | 1 | 8952 | 45842 | 29153 | 9 | NaN |
| 0.0093211 | 1 | 10259 | 44238 | 23.56 | 3 | 0.41856 |
| 0.0025173 | 3 | 16428 | 94911 | 64829 | 1 | 0.80719 |
| 0.0034013 | 1 | 16428 | 94911 | 94911 | 1 | 0.80719 |
| NaN | 0 | NaN | NaN | | 0 | 0.76175 |
| 0.0042698 | 1 | 3455 | 63559 | 63559 | 3 | 0.45162 |
| 0.021922 | 1 | 6779 | 64.82 | 10044 | 1 | |
| 0.00028207 | 1 | 8499 | 106.2 | 76757 | 1 | |
| 0.035698 | 1 | 20837 | 43594 | 15449 | 4 | |
| 0.033141 | 1 | 21255 | 45207 | 17983 | 4 | |
| 0.023274 | 1 | 21859 | 51135 | 17479 | 4 | |
| 0.00011047 | 1 | 10305 | 114.99 | 71032 | 2 | 0.27122 |
| 0.021028 | 1 | 10475 | 90755 | 46157 | 2 | 0.41465 |
| 0.02744 | 1 | 11305 | 128.79 | 86731 | 2 | 0.19931 |
| 0.0087381 | 1 | 5589 | 98077 | 44682 | 2 | 0.42649 |
| 0.00059842 | 1 | 12030 | 103.99 | 70796 | 2 | 0.12084 |
| 0.0099793 | 1 | 5466 | 94973 | 53491 | 2 | 0.12082 |
| 0.16179 | 1 | 13652 | 131.54 | 84649 | 2 | 0.38566 |
| 0.40851 | 1 | 13835 | 125.51 | 65422 | 2 | 0.35571 |
| 0.005735 | 1 | 5602 | 101.23 | 78 | 2 | 0.62417 |
| 7.664E-09 | 1 | 10295 | 154.48 | 111.1 | 2 | 0.27884 |
| 0.0068273 | 2 | 10693 | 139.74 | 84787 | 2 | 0.47856 |
| NaN | 0 | NaN | NaN | | 0 | 0.21525 |
| 0.0027448 | 3 | 5000 | 113.69 | 81986 | 3 | 0.34725 |
| 0.0027173 | 1 | 5304 | 99991 | 75481 | 3 | 0.34253 |
| 0.022825 | 1 | 5646 | 64313 | 50913 | 3 | 0.74067 |
| 0.0024174 | 2 | 5047 | 112.42 | 75976 | 3 | 0.31066 |
| 0.013363 | 1 | 5352 | 69314 | 42956 | 3 | 0.29144 |
| 0.012442 | 1 | 11571 | 70438 | 43549 | 3 | 0.62239 |
| 0.017913 | 1 | 12775 | 48532 | 19229 | 3 | 0.48128 |
| 0.0060641 | 1 | 5110 | 79886 | 54922 | 3 | 0.259 |
| 0.0034134 | 3 | 5036 | 91307 | 61303 | 3 | 0.29809 |
| 0.0036161 | 2 | 5500 | 86803 | 58598 | 3 | 0.2857 |
| NaN | 0 | NaN | NaN | | 0 | 0.46249 |
| 0.032116 | 1 | 21231 | 47225 | 16631 | 6 | |
| 0.006947 | 1 | 7920 | 58635 | 10813 | 5 | NaN |
| 0.01815 | 1 | 4331 | 43635 | 10636 | 1 | 0.4602 |
| NaN | 0 | NaN | NaN | | 0 | 0.53841 |
| 0.0057169 | 1 | 14238 | 65224 | 65947 | 1 | 0.70699 |
| 0.013013 | 1 | 14612 | 54066 | 15763 | 1 | 0.3297 |
| 0.022985 | 1 | 17220 | 57.55 | 11143 | 1 | |
| 0.011181 | 1 | 15899 | 48899 | 96225 | 15 | NaN |
| 0.026132 | 1 | 14173 | 64346 | 42864 | 2 | 0.17971 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.00017333 | 1 | 14967 | | 91414 | 66183 | 2 | 0.24866 |
| 0.0012865 | 1 | 15524 | | 72793 | 53.63 | 2 | 0.11958 |
| 0.0024762 | 1 | 17094 | | 66777 | 66777 | 2 | 0.19281 |
| 0.0046037 | 1 | 14113 | | 60938 | 60938 | 2 | 0.39613 |
| 0.016277 | 1 | 14290 | | 50722 | 31033 | 2 | 0.4492 |
| 0.021213 | 1 | 12473 | | 82267 | 42362 | 2 | 0.53059 |
| 0.0066911 | 1 | 4389 | | 47039 | 15317 | 2 | 0.37845 |
| 0.023679 | 1 | 5542 | | 40767 | 24827 | 2 | 0.47176 |
| 0.0024133 | 1 | 15361 | 56.46 | | 21342 | 4 | 0.53001 |
| 0.0036427 | 1 | 8183 | | 53603 | 35982 | 4 | NaN |
| 0.0037112 | 1 | 12115 | | 53444 | 27084 | 4 | 0.20669 |
| 0.0087212 | 1 | 9313 | | 40086 | 22324 | 4 | 0.32137 |
| 0.012061 | 1 | 16652 | | 48711 | 20774 | 2 | 0.1039 |
| 0.025466 | 1 | 12813 | 46.68 | | 14559 | 1 | NaN |
| 0.0013386 | 1 | 4917 | | 61033 | 33491 | 7 | 0.38502 |
| 0.0053796 | 1 | 13274 | | 55588 | 34365 | 3 | 0.20466 |
| 0.005144 | 1 | 13684 | | 55846 | 32.21 | 3 | 0.28266 |
| 0.0092671 | 1 | 12933 | | 51323 | 30538 | 3 | 0.41583 |
| 0.0084072 | 1 | 16434 | | 61423 | 24478 | 3 | |
| 0.014458 | 1 | 7487 | | 49448 | 23625 | 2 | NaN |
| 0.0089038 | 1 | 14594 | | 40014 | 18742 | 3 | 0.46668 |
| 0.029953 | 1 | 12783 | | 40727 | 14716 | 3 | |
| 0.036037 | 1 | 3027 | | 55176 | 26386 | 4 | 0.91807 |
| 0.0019716 | 1 | 16397 | | 57936 | 31156 | 3 | 0.45789 |
| 0.0081274 | 1 | 12365 | | 50831 | 17164 | 12 | 39502 |
| 0.03808 | 1 | 19987 | | 47548 | 20449 | 1 | |
| 0.018823 | 1 | 16480 | | 45992 | 43487 | 20 | 21.57 |
| 0.020933 | 1 | 1344 | | 51073 | 51073 | 1 | 0.23582 |
| 0.033384 | 1 | 7994 | | 72321 | 24037 | 2 | 31103 |
| 0.018663 | 1 | 8978 | | 62166 | 15.76 | 2 | 12633 |
| 0.0037806 | 1 | 7516 | | 80632 | 50.02 | 2 | 0.33563 |
| 0.030178 | 1 | 13306 | | 48527 | 15167 | 18 | |
| 0.03034 | 1 | 10999 | | 42426 | 8339 | 1 | |
| 0.021587 | 1 | 6160 | | 51727 | 23294 | 6 | |
| 0.012224 | 1 | 9873 | | 61657 | 29935 | 1 | 0.23599 |
| 0.0017606 | 1 | 9712 | 60.55 | | 37177 | 1 | 0.54933 |
| 0.0017005 | 1 | 4387 | | 60968 | 60968 | 1 | 0.53119 |
| 0.041501 | 1 | 17488 | | 45653 | 45653 | 2 | 0.64444 |
| 0.004856 | 1 | 16449 | | 67168 | 43537 | 1 | |
| 0.027041 | 1 | 10809 | | 40616 | 13645 | 1 | 0.55868 |
| 0.0078472 | 1 | 17914 | | 51127 | 24775 | 18 | 0.39556 |
| 0.041501 | 1 | 18042 | | 55437 | 29521 | 18 | 0.59687 |
| 0.038657 | 1 | 9857 | | 78488 | 49699 | 3 | 0.33006 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.0055419 | 1 | 17149 | 53504 | 18175 | 12 | 0.53019 |
| 0.0076226 | 1 | 17537 | 50392 | 21938 | 12 | 0.46746 |
| 0.023386 | 1 | 22392 | 50831 | 33.59 | 45 | |
| 0.030565 | 1 | 13343 | 44511 | 16573 | 9 | 0.94994 |
| 0.014274 | 1 | 15133 | 58658 | 18697 | 9 | 0.37457 |
| NaN | 0 | NaN | NaN | | 0 | 0.43462 |
| NaN | 0 | NaN | NaN | | 0 | 0.52816 |
| NaN | 0 | NaN | NaN | | 0 | 0.24412 |
| 0.0016755 | 1 | 12925 | 53768 | 42309 | 24 | 1123 |
| 0.022349 | 1 | 12925 | 53768 | 42309 | 24 | 1123 |
| 0.0076516 | 1 | 15171 | 54199 | 24262 | 10 | NaN |
| 0.00053114 | 1 | 16570 | 79885 | 39.21 | 20 | NaN |
| 0.0028152 | 1 | 13492 | 65295 | 93153 | 20 | 0.23518 |
| 0.026546 | 1 | 15745 | 55724 | 70125 | 20 | |
| 0.03015 | 1 | 5061 | 41798 | 25389 | 4 | 10127 |
| 0.0080718 | 1 | 10803 | 57434 | 96606 | 2 | 13436 |
| 0.021245 | 1 | 11592 | 42708 | 10757 | 3 | NaN |
| 0.019659 | 1 | 10689 | 56043 | 23825 | 3 | |
| 0.01242 | 1 | 14018 | 46099 | 43611 | 2 | 0.43173 |
| 0.025403 | 1 | 7613 | 44045 | 15496 | 2 | NaN |
| 0.0075169 | 1 | 14614 | 49326 | 27441 | 2 | 0.4862 |
| 0.039358 | 1 | 4281 | 41429 | 11762 | 1 | |
| 0.0062369 | 1 | 7138 | 42863 | 25104 | 4 | 0.2213 |
| 0.00016309 | 1 | 10094 | 80664 | 58.9 | 4 | NaN |
| 0.00035787 | 1 | 10118 | 76807 | 57114 | 4 | 0.26256 |
| 0.94105 | 1 | 6563 | 66845 | 42.34 | 4 | 0.2477 |
| 0.017237 | 1 | 5492 | 78122 | 48897 | 2 | 0.3392 |
| 0.0034438 | 1 | 8025 | 104.57 | 47232 | 2 | NaN |
| 0.039708 | 1 | 12403 | 46145 | 20121 | 1 | |
| 0.03181 | 1 | 17663 | 46701 | 20706 | 1 | |
| 0.03593 | 1 | 15186 | 42095 | 26854 | 1 | |
| 0.005205 | 1 | 10972 | 42059 | 31197 | 2 | 0.37748 |
| 0.36367 | 1 | 13376 | 93196 | 93196 | 1 | 0.31037 |
| 0.0038578 | 1 | 6339 | 47618 | 31603 | 3 | 0.21105 |
| 0.0067692 | 1 | 10542 | 62528 | 26864 | 2 | 26341 |
| 0.0036282 | 1 | 13298 | 44511 | 43821 | 3 | 0.3118 |
| 0.0053608 | 1 | 14997 | 58461 | 32639 | 1 | 0.072178 |
| 0.0043144 | 1 | 14860 | 61765 | 32231 | 9 | 0.61291 |
| 0.023872 | 1 | 5568 | 50831 | 30601 | 3 | 0.41778 |
| 0.018293 | 1 | 6974 | 40602 | 27181 | 3 | 0.5327 |
| 0.0056349 | 2 | 6932 | 48711 | 27745 | 3 | 0.2539 |
| 0.018465 | 1 | 7406 | 54004 | 34831 | 3 | 0.3153 |
| 0.0010818 | 1 | 6609 | 76586 | 54589 | 3 | 0.3185 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0024738 | 3 | 5136 | 56121 | 36823 | 3 | 0.39543 | |
| 8.7414E-07 | 1 | 15498 | 130.52 | 85559 | 1 | 0.6635 | |
| 0.0012285 | 1 | 18618 | 47916 | 14044 | 4 | 0.38902 | |
| 0.024663 | 1 | 7878 | 46337 | 6414 | 3 | 0.010455 | |
| 0.012778 | 1 | 3029 | 51798 | 24468 | 10 | NaN | |
| 0.0041308 | 1 | 7930 | 73168 | 16062 | 4 | | |
| 0.010073 | 1 | 18565 | 42209 | 17754 | 6 | 0.62996 | |
| 0.0074649 | 1 | 22641 | 47499 | 20302 | 20 | NaN | |
| 0.026516 | 1 | 13123 | 40693 | 92128 | 4 | 0.028877 | |
| 0.022886 | 1 | 15476 | 54898 | 81934 | 1 | 43617 | |
| 0.0028271 | 1 | 19458 | 47714 | 24828 | 3 | 0.19781 | |
| 0.023498 | 1 | 13727 | 41164 | 7403 | 4 | NaN | |
| 0.03312 | 1 | 23189 | 42705 | 17973 | 30 | | |
| 0.024206 | 1 | 6117 | 50.04 | 18.72 | 3 | | |
| 0.029653 | 1 | 6034 | 126.03 | 89601 | 2 | 0.31754 | |
| 0.008802 | 1 | 13736 | 53946 | 24223 | 12 | NaN | |
| 0.031088 | 1 | 12520 | 40983 | 14494 | 12 | NaN | |
| 0.013091 | 1 | 21109 | 54953 | 14155 | 6 | | |
| 0.0053845 | 1 | 15022 | 49632 | 31166 | 10 | 0.38472 | |
| 0.0034143 | 1 | 15035 | 68676 | 21971 | 10 | 0.36445 | |
| 0.01108 | 1 | 15998 | 44691 | 11774 | 1 | 0.65746 | |
| 0.0059776 | 1 | 20400 | 59975 | 10759 | 1 | 0.37574 | |
| 0.0074478 | 1 | 11524 | 42818 | 25577 | 10 | 0.61998 | |
| 0.0079764 | 1 | 16454 | 55755 | 21323 | 1 | 0.69976 | |
| NaN | 0 | NaN | NaN | | 0 | 0.43774 | |
| 0.0071909 | 1 | 23301 | 41422 | 14293 | 2 | 0.5331 | |
| 0.039112 | 1 | 16014 | 76818 | 59577 | 5 | 0.38874 | |
| 0.0055099 | 1 | 7239 | 56205 | 11358 | 3 | NaN | |
| 0.020928 | 1 | 6553 | 40242 | 88942 | 3 | NaN | |
| 0.011604 | 1 | 7470 | 47712 | 97173 | 3 | NaN | |
| 0.0041436 | 1 | 9143 | 58885 | 23208 | 3 | 10111 | |
| 0.011975 | 1 | 9484 | 42317 | 72283 | 12 | 0.50548 | |
| 0.02483 | 1 | 7143 | 42802 | 7092 | 2 | | |
| 0.014343 | 1 | 11748 | 44252 | 11745 | 12 | 0.74268 | |
| 0.0099871 | 1 | 12753 | 41621 | 41621 | 12 | 0.64113 | |
| NaN | 0 | NaN | NaN | | 0 | 0.29793 | |
| NaN | 0 | NaN | NaN | | 0 | 0.83982 | |
| 0.0093154 | 1 | 9040 | 44246 | 15175 | 18 | 0.26957 | |
| 0.035826 | 1 | 9568 | 43.69 | 19606 | 18 | 0.60977 | |
| NaN | 0 | NaN | NaN | | 0 | 0.26093 | |
| NaN | 0 | NaN | NaN | | 0 | 10618 | |
| 0.0055019 | 1 | 12566 | 62088 | 29190 | 2 | 60165 | |
| 0.011075 | 1 | 11100 | 54343 | 26289 | 2 | NaN | |

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|---|---|---|---|---|---|---|---|
| 0.0094476 | 1 | 10950 | 56205 | 22.94 | 2 | 14999 | |
| 0.013879 | 1 | 5804 | 51135 | 13958 | 2 | 11805 | |
| 0.013592 | 1 | 12656 | 51463 | 18198 | 2 | 7004 | |
| 0.028261 | 1 | 11531 | 43798 | 68534 | 2 | NaN | |
| 0.014843 | 1 | 11677 | 45207 | 86153 | 6 | 0.47039 | |
| 0.01474 | 1 | 13846 | 50149 | 15648 | 9 | NaN | |
| 0.021143 | 1 | 14537 | 54772 | 19094 | 3 | 0.034462 | |
| 0.026904 | 1 | 12339 | 44.1 | 13856 | 3 | NaN | |
| 0.039301 | 1 | 10876 | 44.98 | 82794 | 1 | 0.6034 | |
| 0.012117 | 1 | 23639 | 43208 | 13605 | 12 | 88539 | |
| 0.00026456 | 2 | 8345 | 60735 | 33549 | 6 | 0.36414 | |
| 0.022045 | 1 | 12101 | 46.88 | 19198 | 2 | 0.37674 | |
| 0.00034151 | 1 | 6543 | 86557 | 67693 | 4 | 0.14147 | |
| 0.004696 | 1 | 15133 | 50255 | 26363 | 4 | NaN | |
| 0.0096204 | 1 | 6510 | 50323 | 22645 | 4 | 0.35956 | |
| 0.01071 | 1 | 9164 | 63419 | 23403 | 2 | 21649 | |
| 0.019139 | 1 | 8014 | 53775 | 23206 | 2 | 29.63 | |
| 0.011481 | 1 | 5455 | 44468 | 27256 | 1 | 0.42219 | |
| 0.011523 | 1 | 6599 | 64749 | 50445 | 1 | 0.449 | |
| 0.0026626 | 1 | 7257 | 55575 | 38.65 | 1 | 0.36541 | |
| 0.0058585 | 1 | 7079 | 72316 | 72316 | 1 | 0.39553 | |
| NaN | 0 | NaN | NaN | | 0 | 0.44217 | |
| 0.004046 | 1 | 3914 | 43.05 | 33.25 | 1 | 0.54788 | |
| 0.0036301 | 1 | 4652 | 43861 | 35553 | 1 | 0.41072 | |
| 0.011728 | 1 | 11251 | 49466 | 23992 | 2 | 0.6584 | |
| 0.021113 | 1 | 10846 | 52167 | 83973 | 2 | | |
| 0.021914 | 1 | 20793 | 41703 | 14432 | 9 | NaN | |
| 0.037809 | 1 | 13799 | 41115 | 10977 | 15 | | |
| 0.041501 | 1 | 7953 | 41621 | 14909 | 3 | NaN | |
| 0.010973 | 1 | 22169 | 43208 | 85592 | 12 | 68372 | |
| 0.0082659 | 1 | 5565 | 68536 | 65775 | 3 | 0.67464 | |
| NaN | 0 | NaN | NaN | | 0 | 0.43249 | |
| 0.0040337 | 1 | 6817 | 41446 | 19745 | 1 | 0.22528 | |
| 0.0010549 | 1 | 9182 | 50178 | 14686 | 1 | 0.093787 | |
| 0.0023183 | 1 | 10573 | 45363 | 26499 | 1 | 0.34137 | |
| 0.033468 | 1 | 8588 | 41429 | 21652 | 1 | | |
| 0.0070692 | 1 | 4275 | 64224 | 81371 | 2 | 0.21532 | |
| 0.0026817 | 1 | 6598 | 75416 | 25933 | 8 | 0.35198 | |
| 0.025354 | 1 | 21535 | 40857 | 20606 | 2 | 0.82051 | |
| 0.032575 | 1 | 14601 | 47537 | 20404 | 3 | 0.40559 | |
| 0.040478 | 1 | 24658 | 43861 | 43861 | 3 | 0.41982 | |
| 0.00035572 | 1 | 11377 | 47376 | 31716 | 2 | 0.17228 | |
| 0.010757 | 2 | 8200 | 51949 | 37.48 | 2 | 0.84105 | |

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|---|---|---|---|---|---|---|
| 0.022437 | 1 | 4435 | 41427 | 18865 | 2 | 0.75432 |
| 0.041501 | 1 | 9477 | 45022 | 20768 | 2 | 0.34812 |
| 0.031613 | 1 | 9855 | 50791 | 16.69 | 5 | 0.41512 |
| 0.0182 | 1 | 7944 | 61815 | 43545 | 2 | NaN |
| 0.011692 | 1 | 8473 | 67214 | 18266 | 2 | NaN |
| 0.011692 | 1 | 8462 | 67214 | 11235 | 2 | 0.086717 |
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| 0.0052422 | 1 | 10100 | 76927 | 32734 | 2 | 0.096784 |
| 0.0059889 | 1 | 6288 | 75416 | 26118 | 2 | 0.01201 |
| 0.0081995 | 1 | 8492 | 70942 | 25289 | 2 | 0.013381 |
| 0.024685 | 1 | 7463 | 58274 | 24187 | 2 | 0.018572 |
| 0.0017384 | 1 | 11862 | 90827 | 56827 | 2 | 0.21213 |
| 0.038559 | 1 | 8382 | 53013 | 68068 | 2 | 0.044513 |
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| 0.0068534 | 1 | 7195 | 73666 | 32283 | 2 | 0.0062677 |
| 0.031417 | 1 | 6332 | 55721 | 20953 | 2 | 0.024096 |
| 0.0001412 | 1 | 17744 | 85805 | 58346 | 2 | 0.26367 |
| 0.0024233 | 2 | 17902 | 62765 | 49076 | 2 | 0.43515 |
| 0.001881 | 1 | 15086 | 96777 | 72423 | 2 | 0.33292 |
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| 0.0054551 | 1 | 10311 | 75738 | 43690 | 1 | 0.67969 |
| 0.012992 | 1 | 10071 | 64.64 | 11403 | 1 | |
| 0.036154 | 1 | 18684 | 44577 | 11436 | 6 | |
| 0.013336 | 1 | 9297 | 50897 | 19282 | 1 | 0.0036227 |
| 0.021134 | 1 | 8342 | 46797 | 25446 | 1 | 0.0074363 |
| 0.0069581 | 2 | 9244 | 61815 | 12621 | 4 | 0.093613 |
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| 0.01719 | 1 | 12242 | 57106 | 19167 | 1 | NaN |
| 0.0032505 | 1 | 9130 | 75739 | 41689 | 1 | 0.33632 |
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| 0.030926 | 1 | 11907 | 42.58 | 19.95 | 3 | 0.71024 |
| 0.034334 | 1 | 9050 | 45368 | 89435 | 4 | 0.17977 |
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| 0.0081741 | 1 | 6673 | 50891 | 21615 | 5 | NaN |
| 0.00022932 | 2 | 9121 | 80314 | 49982 | 5 | 0.43213 |
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| 0.0052321 | 1 | 5346 | 55844 | 30942 | 5 | 0.24467 |
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|---|---|---|---|---|---|---|
| 0.00029277 | 2 | 5360 | 75703 | 50748 | 5 | 0.59265 |
| 0.010752 | 1 | 4126 | 48961 | 25563 | 5 | 0.1266 |
| 0.0044681 | 1 | 12023 | 49066 | 43728 | 12 | 0.69795 |
| 0.010474 | 1 | 16835 | 43042 | 13943 | 12 | 0.42738 |
| 0.0050612 | 1 | 16316 | 47622 | 13729 | 12 | 0.4548 |
| NaN | 0 | NaN | NaN | | 0 | 0.96313 |
| NaN | 0 | NaN | NaN | | 0 | 0.65978 |
| 0.0044329 | 1 | 24986 | 44164 | 18431 | 8 | 0.43339 |
| 0.010467 | 1 | 11468 | 64.82 | 95057 | 6 | 0.39357 |
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| 0.064393 | 1 | 11010 | 63316 | 38686 | 5 | 0.29767 |
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| 0.027894 | 1 | 16020 | 40187 | 12661 | 4 | 0.083061 |
| 0.023762 | 1 | 17589 | 42257 | 17835 | 4 | NaN |
| 0.0047553 | 1 | 19634 | 56872 | 35513 | 4 | 0.052186 |
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| NaN | 0 | NaN | NaN | | 0 | 29714 |
| NaN | 0 | NaN | NaN | | 0 | 12702 |
| 0.038115 | 1 | 3474 | 40154 | 16686 | 3 | |
| 0.022876 | 1 | 9848 | 55064 | 60828 | 2 | |
| 0.0090328 | 1 | 4505 | 84436 | 56117 | 3 | NaN |
| 0.00050631 | 1 | 4212 | 54004 | 54004 | 3 | 0.66971 |
| 0.00014728 | 2 | 4879 | 70316 | 41689 | 3 | 0.60681 |
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| 0.0061945 | 1 | 4148 | 52172 | 23545 | 3 | 0.42382 |
| 0.020574 | 1 | 4797 | 42708 | 20468 | 3 | 0.49494 |
| 0.00013482 | 2 | 5616 | 71376 | 52796 | 3 | 0.84281 |
| 0.0070897 | 1 | 5597 | 50376 | 31796 | 3 | 0.45843 |
| 0.029933 | 1 | 5209 | 71929 | 46772 | 3 | 0.38952 |
| 0.0028963 | 1 | 8664 | 67648 | 42942 | 6 | 0.14313 |
| 0.032513 | 1 | 13479 | 40432 | 21496 | 2 | 0.69025 |
| NaN | 0 | NaN | NaN | | 0 | 0.77178 |
| 0.026547 | 1 | 5129 | 44029 | 24268 | 3 | 0.15335 |
| 0.000655 | 1 | 7126 | 62617 | 41939 | 3 | 0.5177 |
| 0.016141 | 1 | 7635 | 42639 | 22609 | 3 | 0.35349 |
| 0.02124 | 1 | 7642 | 45844 | 28419 | 3 | NaN |
| 0.00062315 | 2 | 4701 | 56748 | 39862 | 3 | 0.63442 |
| 4.3684E-16 | 3 | 21272 | 128.33 | 90339 | 7 | 0.62808 |
| 0.00048003 | 1 | 8209 | 84249 | 66015 | 7 | 0.74161 |
| 0.00020121 | 1 | 8303 | 107.75 | 90506 | 7 | 0.63761 |
| 0.00048098 | 1 | 8283 | 84208 | 84208 | 7 | 0.58945 |
| 0.00045259 | 3 | 20748 | 85423 | 46147 | 7 | 0.55036 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.0034012 | 1 | 19553 | 56719 | 35.15 | 7 | NaN |
| 0.0016868 | 2 | 8222 | 69361 | 69361 | 7 | 0.75594 |
| 6.0305E-16 | 2 | 8373 | 125.73 | 108.49 | 7 | 0.56281 |
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| 0.0035836 | 3 | 21145 | 105.91 | 55867 | 7 | 0.6626 |
| 0.0034179 | 1 | 21208 | 53327 | 24.25 | 7 | 0.28191 |
| 9.3251E-10 | 3 | 24871 | 122.6 | 93847 | 7 | 0.66951 |
| 0.00050727 | 1 | 24926 | 69612 | 46275 | 7 | 0.80047 |
| 3.0081E-07 | 2 | 21071 | 127.49 | 89834 | 7 | 0.42587 |
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| 0.0043172 | 1 | 9764 | 47942 | 22119 | 7 | 0.52528 |
| 0.00061323 | 4 | 8707 | 78552 | 57309 | 7 | 0.62127 |
| 0.00044057 | 5 | 8523 | 85937 | 64364 | 7 | 0.62092 |
| 0.0043557 | 2 | 8539 | 50226 | 29.26 | 7 | 0.35126 |
| 0.00029721 | 2 | 8791 | 85177 | 60509 | 7 | 0.18401 |
| 4.6423E-06 | 9 | 9905 | 115.56 | 89013 | 7 | 0.50312 |
| 0.94809 | 1 | 21020 | 94632 | 76316 | 7 | 0.49387 |
| 0.00046045 | 1 | 16782 | 85087 | 70065 | 7 | 0.39694 |
| 0.00011178 | 5 | 8495 | 111.3 | 72495 | 7 | 0.50955 |
| 0.00020613 | 4 | 8376 | 91926 | 74207 | 7 | 0.50597 |
| 0.0076101 | 1 | 8395 | 58864 | 30698 | 7 | |
| 0.22873 | 1 | 8671 | 97271 | 82391 | 7 | 0.35501 |
| NaN | 0 | | NaN | NaN | 0 | 0.69868 |
| 0.0099691 | 1 | 13639 | 47016 | 64696 | 8 | 0.5026 |
| 0.020133 | 1 | 5593 | 41257 | 18627 | 6 | 0.25871 |
| 0.016457 | 1 | 8863 | 43091 | 25076 | 6 | NaN |
| 0.0021378 | 1 | 5542 | 50358 | 21809 | 6 | 0.46976 |
| 0.024512 | 1 | 23661 | 47187 | 14.62 | 1 | |
| 0.00060368 | 1 | 6010 | 71685 | 39494 | 3 | 0.39278 |
| 0.0045191 | 2 | 15975 | 68676 | 44269 | 2 | 0.63431 |
| 0.0027084 | 2 | 7149 | 66041 | 33.95 | 2 | 0.37721 |
| 0.024744 | 1 | 7074 | 86179 | 86179 | 2 | 0.7238 |
| NaN | 0 | | NaN | NaN | 0 | 0.53294 |
| 0.0041788 | 1 | 13639 | 40798 | 79401 | 42 | 0.33531 |
| 0.013928 | 1 | 14309 | 40177 | 20.83 | 21 | 0.48278 |
| NaN | 0 | | NaN | NaN | 0 | 0.48512 |
| 0.026924 | 1 | 10724 | 45357 | 12927 | 3 | NaN |
| 0.016234 | 1 | 12035 | 52579 | 65772 | 3 | |
| 0.029975 | 1 | 4702 | 65465 | 14213 | 3 | 0.18581 |
| 0.030294 | 1 | 15787 | 88283 | 41486 | 3 | 0.17475 |
| 0.021733 | 2 | 7087 | 90385 | 63123 | 3 | 0.27006 |
| 0.035888 | 1 | 14615 | 87676 | 60413 | 3 | 0.24707 |
| 0.0061697 | 1 | 13851 | 100.77 | 84926 | 3 | 0.8397 |

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|---|---|---|---|---|---|---|---|
| 0.0022498 | 1 | 6811 | 104.88 | | 89939 | 3 | 0.30248 |
| 0.0065927 | 1 | 8043 | | 69581 | 69581 | 3 | 0.27591 |
| 0.031 | 1 | 11864 | | 52008 | 67278 | 18 | |
| 0.018399 | 1 | 19406 | | 58592 | 17598 | 1 | |
| 0.030004 | 1 | 11763 | | 45653 | 22293 | 15 | |
| 0.030708 | 1 | 9603 | 46.89 | | 75515 | 10 | |
| 0.005004 | 1 | 13742 | | 95429 | 50989 | 80 | NaN |
| 0.0097054 | 2 | 7441 | | 51104 | 31948 | 3 | 0.33058 |
| 0.86601 | 1 | 5983 | 106.31 | | 85721 | 3 | 0.96199 |
| 0.18711 | 1 | 5785 | 113.86 | | 97118 | 3 | 0.26731 |
| 0.0017519 | 1 | 5830 | | 89913 | 69677 | 3 | 0.38826 |
| 0.0023236 | 2 | 5682 | | 85046 | 67418 | 3 | 0.50712 |
| 0.0045983 | 1 | 18690 | 47.05 | | 21126 | 45 | NaN |
| 0.038563 | 1 | 7996 | | 41427 | 17195 | 2 | 0.20728 |
| 0.011363 | 1 | 15517 | | 59884 | 33112 | 3 | |
| 0.011712 | 1 | 18688 | | 51469 | 32533 | 7 | 0.51866 |
| 0.0043264 | 1 | 12296 | | 40986 | 12895 | 35 | 0.35024 |
| 0.032187 | 1 | 4718 | | 45115 | 14257 | 3 | NaN |
| 0.0060348 | 1 | 15472 | | 63181 | 13847 | 2 | 13046 |
| 0.039321 | 1 | 24020 | | 58172 | 87241 | 6 | NaN |
| 0.011627 | 1 | 1240 | | 42629 | 30571 | 4 | 0.58787 |
| 0.0021129 | 2 | 1671 | | 58274 | 47348 | 4 | 0.48042 |
| 0.0020297 | 1 | 18544 | | 49497 | 75857 | 30 | 39007 |
| 0.003254 | 1 | 10400 | | 61161 | 85827 | 2 | 0.60011 |
| 0.00011073 | 1 | 17054 | | 63925 | 39718 | 3 | 0.47343 |
| 0.00041089 | 2 | 16830 | | 82942 | 82942 | 3 | NaN |
| 0.0030549 | 1 | 15804 | 47.05 | | 27121 | 3 | 0.61585 |
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| 0.040158 | 2 | 18880 | | 57629 | 41819 | 2 | 0.2115 |
| 0.03597 | 1 | 4781 | | 48907 | 25916 | 3 | 0.29631 |
| 0.0090881 | 1 | 7651 | | 65887 | 46124 | 5 | 0.2541 |
| 0.013697 | 1 | 6573 | | 62002 | 48379 | 5 | 0.44899 |
| 0.0025483 | 1 | 13644 | | 47548 | 16.41 | 4 | 0.5026 |
| 0.0068367 | 1 | 20960 | | 42314 | 13982 | 4 | 0.32278 |
| 0.0070169 | 1 | 20592 | | 42095 | 26493 | 4 | 0.57424 |
| 0.03068 | 1 | 22205 | | 40103 | 12983 | 5 | NaN |
| 0.0033688 | 1 | 5888 | | 52966 | 67171 | 6 | 0.4069 |
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| NaN | 0 | NaN | | NaN | | 0 | 0.34407 |
| 0.024356 | 1 | 10768 | | 61765 | 20656 | 2 | |
| 0.028584 | 1 | 11840 | | 86803 | 67506 | 3 | 0.4286 |
| 0.024336 | 1 | 10297 | 89.44 | | 42378 | 3 | 0.3455 |

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|---|---|---|---|---|---|---|
| 0.0069893 | 1 | 12360 | 45084 | 19102 | 1 | 0.43579 |
| 0.0025547 | 1 | 10770 | 54103 | 27742 | 3 | 0.73698 |
| 0.0028601 | 1 | 11365 | 52814 | 24459 | 3 | 0.032076 |
| 0.02981 | 1 | 20702 | 77288 | 51.17 | 2 | 0.49286 |
| NaN | 0 | NaN | NaN | | 0 | 0.47535 |
| 0.025826 | 1 | 10358 | 56916 | 14705 | 3 | |
| 0.0068009 | 1 | 10752 | 63624 | 24 | 6 | NaN |
| 0.004607 | 1 | 10195 | 70942 | 7761 | 2 | NaN |
| 0.034442 | 1 | 8310 | 57047 | 21603 | 2 | 0.044587 |
| 0.0095447 | 1 | 13692 | 62077 | 26979 | 16 | 29426 |
| 0.0075079 | 1 | 13370 | 53377 | 86432 | 2 | 0.19195 |
| 0.010466 | 1 | 14965 | 47726 | 61113 | 8 | NaN |

| Ratio H/L nor | Ratio H/L shif | Intensity | Intensity L | Intensity H | Reverse | Potential con |
|---|---|---|---|---|---|---|
| 0.57984 | 0 | 119240 | 84688 | 34548 | | |
| 0.73098 | 0 | 88880 | 65772 | 23108 | | |
| 0.35155 | 0 | 247460 | 209250 | 38214 | | |
| 0.53892 | 0 | 229620 | 176360 | 53258 | | |
| 0.51506 | 0 | 164080 | 137950 | 26132 | | |
| 0.28614 | 0 | 192690 | 172720 | 19962 | | |
| 0.44277 | 0 | 84864 | 78384 | 6480.6 | | |
| 0.25798 | 0 | 90922 | 75426 | 15496 | | |
| 0.38091 | 0 | 67903 | 46479 | 21424 | | |
| 12628 | 0 | 173700 | 12556 | 161150 | | |
| NaN | 0 | 142390 | 141990 | 407.64 | | |
| 0.94138 | 0 | 313510 | 204840 | 108670 | | |
| 14614 | 0 | 218980 | 132170 | 86805 | | |
| NaN | 0 | 105780 | 98411 | 7367.4 | | |
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| 10247 | 0 | 313690 | 179890 | 133790 | | |
| 0.86522 | 0 | 578820 | 331790 | 247040 | | |
| 12257 | 0 | 756200 | 447440 | 308760 | | |
| 0.65471 | 0 | 401910 | 277420 | 124490 | | |
| 0.90773 | 0 | 4876900 | 2849900 | 2027100 | | |
| 21426 | 0 | 813590 | 481360 | 332230 | | |
| 0.45693 | 0 | 129650 | 112250 | 17405 | | |
| 0.97177 | 0 | 707250 | 476140 | 231110 | | |
| 0.90304 | 0 | 339740 | 185380 | 154350 | | |
| 1655 | 0 | 114740 | 45031 | 69710 | | |
| 13952 | 0 | 156460 | 80831 | 75629 | | |
| 10078 | 0 | 359240 | 234560 | 124680 | | |
| | | | | | | |
| 11573 | 0 | 242390 | 145890 | 96503 | | |
| 0.93693 | 0 | 80759 | 49713 | 31047 | | |
| 0.87588 | 0 | 137250 | 112380 | 24868 | | |
| 13616 | 0 | 599260 | 339050 | 260210 | | |
| 13431 | 0 | 273570 | 164130 | 109440 | | |
| 0.49196 | 0 | 90726 | 55894 | 34831 | | |
| 11528 | 0 | 132120 | 81066 | 51050 | | |
| 10819 | 0 | 65880 | 44312 | 21569 | | |
| 0.21051 | 0 | 289450 | 271610 | 17837 | | |
| 0.15605 | 0 | 231540 | 220620 | 10918 | | |
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|---|---|---|---|---|---|
| NaN | 0 | 948710 | 618890 | 329820 | |
| 0.65032 | 0 | 533560 | 408580 | 124980 | |
| 10214 | 0 | 7382900 | 3846400 | 3536400 | + |
| 10214 | 0 | 7382900 | 3846400 | 3536400 | + |
| 12928 | 0 | 63270 | 43570 | 19700 | + |
| 0.69503 | 0 | 91083 | 60678 | 30406 | |
| | | | | | |
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| | | | | | |
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| 0.50367 | 0 | 255820 | 208970 | 46851 | |
| 0.68522 | 0 | 120480 | 85761 | 34715 | |
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| 0.57834 | 0 | 215610 | 156630 | 58975 | |
| 0.29314 | 0 | 165720 | 146660 | 19056 | |
| 0.11562 | 0 | 61337 | 54770 | 6566.9 | |
| 0.78028 | 0 | 309790 | 261000 | 48791 | |
| 0.67052 | 0 | 567380 | 403460 | 163920 | |
| 1057 | 0 | 122240 | 78061 | 44174 | |
| 0.76923 | 0 | 259970 | 200520 | 59452 | |
| 10578 | 0 | 255800 | 185350 | 70457 | |
| 0.37952 | 0 | 90624 | 68113 | 22511 | |
| 0.68932 | 0 | 1099700 | 782150 | 317510 | |
| 0.32049 | 0 | 288330 | 210060 | 78265 | |
| 0.85198 | 0 | 92724 | 53318 | 39407 | |
| 0.47149 | 0 | 1000500 | 723220 | 277270 | |
| 0.38078 | 0 | 175680 | 126400 | 49279 | |
| 12283 | 0 | 226430 | 135120 | 91304 | |
| 0.92394 | 0 | 245390 | 165200 | 80189 | |
| 0.56326 | 0 | 91162 | 73823 | 17339 | |
| 0.67576 | 0 | 1507900 | 1142600 | 365350 | |
| 0.67518 | 0 | 313510 | 226040 | 87470 | |
| 0.9039 | 0 | 216730 | 144730 | 72005 | |
| | | | | | |
| NaN | 0 | 175250 | 2451.8 | 172800 | |
| 0.70272 | 0 | 141990 | 90082 | 51908 | |
| 0.42025 | 0 | 65000 | 39535 | 25465 | |
| 1205 | 0 | 249100 | 134730 | 114360 | |
| 0.71817 | 0 | 101870 | 78338 | 23527 | |
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| NaN | 0 | 49661 | 0 | 49661 | |
| 0.29435 | 0 | 222970 | 194040 | 28930 | |

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|---|---|---|---|---|
| 0.44968 | 0 | 563920 | 450140 | 113770 |
| 0.29647 | 0 | 412880 | 368280 | 44599 |
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| 1103 | 0 | 233860 | 170080 | 63786 |
| 0.99748 | 0 | 348080 | 237670 | 110410 |
| 10496 | 0 | 233940 | 157990 | 75949 |
| 0.71628 | 0 | 290030 | 203570 | 86459 |
| 0.96139 | 0 | 334750 | 215590 | 119160 |
| 0.94173 | 0 | 155670 | 108410 | 47258 |
| NaN | 0 | 46427 | 46427 | 0 |
| 0.42529 | 0 | 224170 | 173460 | 50716 |
| 0.49948 | 0 | 144360 | 94052 | 50313 |
| 0.1674 | 0 | 583050 | 492700 | 90355 |
| NaN | 0 | 169030 | 7818.4 | 161210 |
| 0.46507 | 0 | 141240 | 93405 | 47837 |
| 0.50514 | 0 | 566310 | 504650 | 61657 |
| 0.51941 | 0 | 3542300 | 3076600 | 465680 |
| 0.8704 | 0 | 940910 | 803650 | 137260 |
| | | | | |
| NaN | 0 | 127550 | 127550 | 0 |
| 1118 | 0 | 225000 | 141650 | 83349 |
| | | | | |
| 21855 | 0 | 129210 | 66144 | 63070 |
| 0.43474 | 0 | 781810 | 449920 | 331890 |
| 69727 | 0 | 673200 | 126020 | 547180 |
| | | | | |
| 43778 | 0 | 405010 | 21418 | 383590 |
| 0.31421 | 0 | 51616 | 38672 | 12944 |
| 56773 | 0 | 61882 | 10820 | 51062 |
| 23934 | 0 | 141910 | 51627 | 90278 |
| 0.72155 | 0 | 59383 | 43312 | 16070 |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| 0.44605 | 0 | 52323 | 47569 | 4753.8 |
| 10384 | 0 | 63053 | 37972 | 25081 |
| 0.41515 | 0 | 48416 | 32483 | 15933 |
| 13198 | 0 | 257740 | 168290 | 89450 |
| | | | | |
| 10617 | 0 | 82681 | 54727 | 27953 |
| 0.80221 | 0 | 267730 | 199900 | 67833 |
| 11831 | 0 | 235780 | 146960 | 88819 |
| 0.62867 | 0 | 192830 | 140670 | 52161 |
| | | | | |
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|---|---|---|---|---|---|---|
| 0.872 | 0 | 1201900 | 614420 | 587520 | | + |
| 11019 | 0 | 382440 | 233280 | 149170 | | + |
| | | | | | | |
| 12567 | 0 | 4788200 | 2287400 | 2500800 | + | |
| 0.60287 | 0 | 5225400 | 3739200 | 1486200 | + | |
| 0.73885 | 0 | 40278 | 24927 | 15351 | + | |
| 0.95139 | 0 | 17833000 | 10411000 | 7421600 | + | |
| 0.47429 | 0 | 269230 | 216790 | 52439 | + | |
| 20359 | 0 | 1336400 | 547220 | 789140 | + | |
| 20359 | 0 | 1336400 | 547220 | 789140 | + | |
| NaN | 0 | 75545 | 3620.3 | 71925 | | |
| NaN | 0 | 118170 | 113950 | 4228.6 | | |
| 0.47712 | 0 | 704450 | 583790 | 120660 | | |
| | | | | | | |
| 19572 | 0 | 80164 | 43221 | 36943 | | |
| 20773 | 0 | 549530 | 258330 | 291210 | | |
| NaN | 0 | 118510 | 117450 | 1068.2 | | |
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| 0.68091 | 0 | 81763 | 56657 | 25106 | | |
| NaN | 0 | 38095 | 38095 | 0 | | |
| 10889 | 0 | 88606 | 56127 | 32479 | | |
| | | | | | | |
| 0.25037 | 0 | 92069 | 79289 | 12781 | | |
| NaN | 0 | 2094800 | 1472500 | 622330 | | |
| 0.36563 | 0 | 1630400 | 1123800 | 506620 | | |
| 0.32395 | 0 | 109120 | 94661 | 14462 | | |
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| NaN | 0 | 224060 | 210040 | 14027 | | + |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| | | | | | | |
| 0.8344 | 0 | 107580 | 74859 | 32725 | | |
| 0.42549 | 0 | 1130200 | 837440 | 292760 | | |
| 0.41441 | 0 | 131510 | 106460 | 25052 | | |
| 58018 | 0 | 262860 | 9999.3 | 252860 | | |
| 0.72226 | 0 | 612300 | 522560 | 89737 | | |
| 0.081851 | 0 | 248790 | 226140 | 22648 | | |
| 10226 | 0 | 2609100 | 1567300 | 1041800 | | |
| 0.83063 | 0 | 70607 | 51988 | 18619 | | |
| 1167 | 0 | 85966 | 59484 | 26482 | | |
| 0.17394 | 0 | 142560 | 96229 | 46327 | | |
| 0.61909 | 0 | 112590 | 76884 | 35704 | | |
| 0.51276 | 0 | 145510 | 109250 | 36260 | | |

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|---|---|---|---|---|---|
| 0.74773 | 0 | 259730 | 179230 | 80499 | |
| 14503 | 0 | 124760 | 77149 | 47611 | |
| 0.35248 | 0 | 596300 | 456280 | 140020 | + |
| 0.010883 | 0 | 1484100 | 1470600 | 13541 | |
| NaN | 0 | 47083 | 0 | 47083 | |
| | | | | | |
| 12824 | 0 | 3488800 | 2057200 | 1431700 | |
| NaN | 0 | 111000 | 0 | 111000 | |
| 0.060171 | 0 | 3534500 | 3438100 | 96399 | |
| 22121 | 0 | 307820 | 146820 | 161000 | |
| 0.40595 | 0 | 202890 | 179410 | 23481 | |
| NaN | 0 | 186780 | 184800 | 1975.3 | |
| | | | | | |
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| 0.59997 | 0 | 126640 | 90471 | 36171 | |
| NaN | 0 | 320330 | 320330 | 0 | |
| NaN | 0 | 100890 | 95525 | 5365.8 | |
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| 0.76132 | 0 | 644980 | 482650 | 162320 | |
| 0.69286 | 0 | 477550 | 373400 | 104150 | |
| 12879 | 0 | 190470 | 103230 | 87242 | |
| 0.37879 | 0 | 1415900 | 1036800 | 379070 | + |
| 11306 | 0 | 1152000 | 692920 | 459080 | |
| 13769 | 0 | 140760 | 85807 | 54957 | |
| 0.88871 | 0 | 138730 | 80715 | 58018 | |
| 10384 | 0 | 908070 | 538680 | 369390 | |
| 0.73671 | 0 | 158880 | 119960 | 38917 | |
| NaN | 0 | 579630 | 0 | 579630 | |
| NaN | 0 | 1413400 | 5969.9 | 1407400 | |
| NaN | 0 | 1577100 | 2660.6 | 1574400 | |
| 16106 | 0 | 1761700 | 199790 | 1561900 | |
| 0.69084 | 0 | 152640 | 91267 | 61377 | |
| | | | | | |
| 13636 | 0 | 222500 | 143610 | 78888 | |
| 0.99817 | 0 | 747460 | 411250 | 336210 | |
| 0.71009 | 0 | 2616300 | 1958600 | 657700 | |
| 12681 | 0 | 157470 | 77181 | 80285 | |
| 0.67044 | 0 | 588100 | 436040 | 152060 | |
| 11169 | 0 | 64518 | 45510 | 19007 | |
| 0.64895 | 0 | 231730 | 175970 | 55754 | |
| 16839 | 0 | 75448 | 41623 | 33824 | |
| 10579 | 0 | 177870 | 20506 | 157370 | |
| NaN | 0 | 141500 | 3165.4 | 138330 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 29139 | 0 | 155890 | 6584.4 | 149300 | |
| | 12805 | 0 | 245330 | 6144.9 | 239180 | |
| | 13609 | 0 | 274210 | 11373 | 262840 | |
| NaN | | 0 | 557620 | 8397 | 549220 | |
| | 10329 | 0 | 387120 | 326370 | 60754 | |
| NaN | | 0 | 150110 | 150110 | 0 | |
| 0.071051 | | 0 | 458210 | 447510 | 10695 | |
| NaN | | 0 | 44137 | 44137 | 0 | |
| | 11035 | 0 | 54728 | 33299 | 21429 | |
| | 14984 | 0 | 159940 | 9393.4 | 150550 | + |
| 0.61664 | | 0 | 119030 | 88874 | 30154 | |
| 0.69043 | | 0 | 232280 | 168040 | 64239 | |
| 0.13002 | | 0 | 68358 | 62946 | 5411.8 | |
| NaN | | 0 | 82502 | 76424 | 6077.1 | |
| 0.81089 | | 0 | 187560 | 116680 | 70873 | |
| | 41549 | 0 | 259330 | 8189.1 | 251140 | |
| | 66059 | 0 | 458870 | 19718 | 439150 | |
| 0.85524 | | 0 | 125600 | 83931 | 41672 | |
| | 10192 | 0 | 79361 | 56407 | 22954 | |
| 0.73437 | | 0 | 148100 | 96002 | 52094 | |
| 0.77457 | | 0 | 121610 | 85316 | 36293 | |
| 0.74515 | | 0 | 86893 | 58523 | 28370 | |
| 0.7399 | | 0 | 145970 | 95549 | 50423 | |
| 0.57051 | | 0 | 169540 | 106950 | 62587 | |
| | 13895 | 0 | 3667900 | 2133300 | 1534600 | |
| | | | | | | |
| NaN | | 0 | 313750 | 311870 | 1886.5 | |
| | | | | | | |
| NaN | | 0 | 48021 | 0 | 48021 | + |
| | 32448 | 0 | 117830 | 5923.9 | 111900 | |
| | 13252 | 0 | 611770 | 421080 | 190690 | |
| 0.83229 | | 0 | 365160 | 284700 | 80454 | |
| 0.32425 | | 0 | 98676 | 80919 | 17757 | |
| 0.10636 | | 0 | 177240 | 151810 | 25433 | |
| 0.4312 | | 0 | 397460 | 267310 | 130150 | |
| | | | | | | |
| 0.33156 | | 0 | 2454400 | 2047800 | 406530 | |
| 0.62262 | | 0 | 187470 | 133590 | 53884 | |
| | 14833 | 0 | 202480 | 113830 | 88643 | |
| 0.4546 | | 0 | 225420 | 165180 | 60239 | |
| 0.8017 | | 0 | 2313800 | 1693400 | 620410 | |
| 0.32468 | | 0 | 341520 | 318030 | 23491 | |
| | 13087 | 0 | 521720 | 258180 | 263540 | |

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|---|---|---|---|---|
| 14326 | 0 | 108750 | 61541 | 47204 |
| 0.77004 | 0 | 171740 | 103250 | 68490 |
| 0.92008 | 0 | 211480 | 134120 | 77361 |
| NaN | 0 | 577970 | 576350 | 1613.4 |
| NaN | 0 | 653230 | 653230 | 0 |
| 0.1509 | 0 | 555960 | 531660 | 24302 |
| NaN | 0 | 161320 | 161320 | 0 |
| 0.15305 | 0 | 144570 | 125540 | 19027 |
| 0.014556 | 0 | 428150 | 424920 | 3227.6 |
| 0.030196 | 0 | 1422400 | 1411100 | 11342 |
| 0.029208 | 0 | 891850 | 884880 | 6971.7 |
| 0.36952 | 0 | 262100 | 211230 | 50870 |
| 0.088132 | 0 | 236880 | 231360 | 5519.7 |
| NaN | 0 | 1002300 | 1002300 | 0 |
| 0.0317 | 0 | 2060000 | 2043500 | 16450 |
| NaN | 0 | 2216100 | 2162400 | 53705 |
| 0.1905 | 0 | 91803 | 87186 | 4617 |
| 0.25369 | 0 | 133890 | 120940 | 12953 |
| 0.10484 | 0 | 239590 | 221720 | 17874 |
| 0.017454 | 0 | 1062000 | 1053200 | 8798.7 |
| 0.051932 | 0 | 335180 | 326930 | 8245.6 |
| 0.4968 | 0 | 69172 | 54664 | 14508 |
| 0.79754 | 0 | 113370 | 80653 | 32720 |
| 0.65676 | 0 | 139310 | 108980 | 30327 |
| 0.76525 | 0 | 181360 | 123370 | 57998 |
| 10179 | 0 | 1443800 | 819400 | 624370 |
| | | | | |
| | | | | |
| 0.0064642 | 0 | 3335500 | 3323200 | 12336 |
| 0.016191 | 0 | 2656100 | 2623500 | 32549 |
| 0.11846 | 0 | 128180 | 114280 | 13898 |
| 318.97 | 0 | 2251000 | 7626.7 | 2243400 |
| NaN | 0 | 135490 | 131270 | 4217.9 |
| 0.75764 | 0 | 654530 | 498160 | 156370 |
| NaN | 0 | 233020 | 229570 | 3453.5 |
| 11517 | 0 | 85258 | 40973 | 44285 |
| 0.34706 | 0 | 103430 | 85063 | 18368 |
| NaN | 0 | 92543 | 77324 | 15219 |
| NaN | 0 | 60116 | 54471 | 5645.3 |
| 0.84281 | 0 | 878720 | 613020 | 265710 |
| 13479 | 0 | 642750 | 380090 | 262660 |
| 0.42285 | 0 | 49295 | 41142 | 8152.9 |
| 1242 | 0 | 505290 | 318400 | 186890 |

| | | | | | |
|---|---|---|---|---|---|
| 12257 | 0 | 533460 | 308040 | 225410 | |
| 0.26813 | 0 | 56813 | 52924 | 3888.9 | |
| 12661 | 0 | 894260 | 458810 | 435450 | |
| 10955 | 0 | 4374300 | 2900300 | 1474000 | |
| 10781 | 0 | 13491000 | 8835000 | 4656400 | |
| 14941 | 0 | 706560 | 347160 | 359400 | |
| 0.97956 | 0 | 188160 | 115920 | 72239 | |
| 0.82848 | 0 | 1786700 | 1214900 | 571820 | |
| 0.85365 | 0 | 116440 | 74135 | 42301 | + |
| 0.81982 | 0 | 406320 | 289960 | 116360 | + |
| 0.57508 | 0 | 237170 | 210870 | 26301 | |
| 0.34073 | 0 | 1303500 | 1163800 | 139640 | |
| 0.51493 | 0 | 143060 | 124400 | 18659 | |
| 0.16536 | 0 | 100850 | 93220 | 7629.4 | |
| NaN | 0 | 46745 | 46745 | 0 | |
| 0.10315 | 0 | 116880 | 108830 | 8055.2 | |
| 1357 | 0 | 249070 | 180500 | 68576 | |
| 43652 | 0 | 56003 | 19347 | 36656 | |
| 30894 | 0 | 128600 | 55043 | 73552 | |

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|---|---|---|---|---|---|
| NaN | 0 | 52078 | 52078 | 0 | |
| 0.93025 | 0 | 211160 | 114800 | 96363 | |
| 1012 | 0 | 89692 | 52988 | 36704 | |
| 13021 | 0 | 251520 | 141240 | 110280 | |
| 0.6305 | 0 | 114300 | 70632 | 43672 | |
| 0.79741 | 0 | 82466 | 60394 | 22072 | |
| 10646 | 0 | 106460 | 65136 | 41320 | |
| 0.57906 | 0 | 158280 | 103420 | 54860 | |
| 0.40049 | 0 | 89313 | 71397 | 17916 | |
| 0.27545 | 0 | 123560 | 105430 | 18134 | |
| 13324 | 0 | 228190 | 140540 | 87655 | |
| 15523 | 0 | 219220 | 135430 | 83788 | |
| 0.29128 | 0 | 89001 | 74059 | 14942 | |
| 10412 | 0 | 818880 | 487590 | 331290 | |
| 0.66225 | 0 | 654380 | 444330 | 210050 | |
| NaN | 0 | 64862 | 64862 | 0 | |
| 14904 | 0 | 266300 | 165400 | 100900 | |
| 10051 | 0 | 1901500 | 1090500 | 810990 | |
| 0.68158 | 0 | 1453600 | 805760 | 647870 | |
| 0.95864 | 0 | 1158400 | 695120 | 463320 | |
| 0.58697 | 0 | 59934 | 36716 | 23218 | |
| 14178 | 0 | 2026200 | 1208300 | 817880 | |

| | | | | |
|---|---|---|---|---|
| NaN | 0 | 43166 | 43166 | 0 |
| 0.72339 | 0 | 124750 | 78014 | 46734 |
| 0.62984 | 0 | 2941100 | 1794600 | 1146500 |
| 0.42596 | 0 | 64606 | 42323 | 22282 |
| 12529 | 0 | 2618500 | 1571500 | 1047100 |
| 0.53131 | 0 | 156910 | 135450 | 21458 |
| 12766 | 0 | 3915700 | 2315200 | 1600500 |
| 15623 | 0 | 289850 | 153280 | 136570 |
| 0.82121 | 0 | 242170 | 179200 | 62965 |
| 11689 | 0 | 655680 | 391280 | 264400 |
| 0.92615 | 0 | 102710 | 69948 | 32766 |
| 11579 | 0 | 453040 | 255010 | 198030 |
| 0.9251 | 0 | 466950 | 286540 | 180400 |
| 0.52334 | 0 | 88476 | 53149 | 35327 |
| 0.2921 | 0 | 151450 | 128630 | 22816 |
| 10846 | 0 | 542010 | 365290 | 176720 |
| 10295 | 0 | 296540 | 200440 | 96097 |
| 0.87918 | 0 | 120580 | 86476 | 34104 |
| 11492 | 0 | 5734100 | 3887800 | 1846300 |
| 0.61117 | 0 | 687410 | 446820 | 240590 |
| | | | | |
| 0.29377 | 0 | 99281 | 75588 | 23692 |
| 12254 | 0 | 774480 | 428530 | 345950 |
| 0.87354 | 0 | 7494700 | 4706300 | 2788400 |
| 0.50847 | 0 | 91224 | 64874 | 26350 |
| NaN | 0 | 56240 | 56240 | 0 |
| 10216 | 0 | 91211 | 60358 | 30854 |
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| 0.39112 | 0 | 82211 | 54581 | 27630 |
| 12041 | 0 | 117670 | 75292 | 42381 |
| 0.59879 | 0 | 97113 | 73418 | 23694 |
| 16323 | 0 | 111800 | 61253 | 50550 |
| 0.64375 | 0 | 57473 | 34715 | 22758 |
| 0.61329 | 0 | 1748100 | 1130500 | 617610 |
| 0.92336 | 0 | 450530 | 270420 | 180110 |
| 0.83099 | 0 | 85263 | 56504 | 28758 |
| NaN | 0 | 176580 | 176580 | 0 |
| | | | | |
| 0.4475 | 0 | 1499900 | 1216300 | 283670 |
| 0.34132 | 0 | 101060 | 82624 | 18433 |
| 0.45734 | 0 | 108830 | 63209 | 45622 |
| 0.64593 | 0 | 75413 | 67108 | 8304.4 |
| 18009 | 0 | 78514 | 40108 | 38407 |

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|---|---|---|---|---|
| 0.68216 | 0 | 64185 | 49273 | 14912 |
| 0.62224 | 0 | 64049 | 44530 | 19519 |
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| | | | | |
| | | | | |
| NaN | 0 | 837990 | 19039 | 818950 |
| 0.39931 | 0 | 125680 | 86590 | 39089 |
| 13045 | 0 | 87666 | 49634 | 38032 |
| 0.29914 | 0 | 55770 | 45824 | 9946.3 |
| 0.8756 | 0 | 82492 | 53913 | 28579 |
| 0.61257 | 0 | 207700 | 126640 | 81057 |
| NaN | 0 | 94214 | 88359 | 5854.6 |
| 0.34568 | 0 | 109580 | 86096 | 23483 |
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| 0.89241 | 0 | 69319 | 38710 | 30608 |
| 0.76746 | 0 | 847080 | 548680 | 298400 |
| NaN | 0 | 34744 | 34744 | 0 |
| 31742 | 0 | 523030 | 229990 | 293040 |
| NaN | 0 | 79469 | 10386 | 69083 |
| 0.89905 | 0 | 78222 | 47782 | 30441 |
| 0.65496 | 0 | 132780 | 102620 | 30154 |
| 75071 | 0 | 2114000 | 12211 | 2101800 |
| 14294 | 0 | 130280 | 106460 | 23818 |
| 0.84009 | 0 | 364630 | 295410 | 69226 |
| NaN | 0 | 740550 | 424140 | 316410 |
| 12631 | 0 | 137830 | 80739 | 57090 |
| 0.28587 | 0 | 836310 | 771380 | 64928 |
| 0.592 | 0 | 448200 | 395640 | 52557 |
| 0.4054 | 0 | 333960 | 290510 | 43447 |
| 0.20262 | 0 | 117810 | 88093 | 29718 |
| 0.43587 | 0 | 351840 | 258410 | 93431 |
| 0.97087 | 0 | 168420 | 120150 | 48273 |
| 0.87354 | 0 | 7494700 | 4706300 | 2788400 |
| 0.82022 | 0 | 1078500 | 800280 | 278240 |
| 11467 | 0 | 272680 | 166300 | 106380 |
| NaN | 0 | 38699 | 38699 | 0 |
| 0.97218 | 0 | 671810 | 442000 | 229820 |
| 0.2469 | 0 | 117060 | 85168 | 31896 |
| 0.43461 | 0 | 144390 | 84054 | 60331 |
| | | | | |
| 0.83926 | 0 | 256160 | 168910 | 87249 |
| 0.74264 | 0 | 157100 | 112620 | 44478 |
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| | | | | |
| | | | | |
| | | | | |

| | | | | | |
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| 0.81733 | 0 | 336610 | 217500 | 119120 | |
| 16722 | 0 | 386060 | 217020 | 169040 | + |
| 0.067382 | 0 | 336330 | 318230 | 18107 | + |
| 0.91535 | 0 | 105040 | 61200 | 43838 | |
| 0.8915 | 0 | 93792 | 62280 | 31512 | |
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| NaN | 0 | 95492 | 89944 | 5547.4 | |
| NaN | 0 | 69439 | 65853 | 3586.1 | |
| 0.096657 | 0 | 145340 | 140920 | 4415.4 | |
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| 0.35652 | 0 | 363290 | 293900 | 69385 | |
| NaN | 0 | 203840 | 4208.4 | 199630 | |

| id | Protein group | Peptide ID | Mod. peptide | MS/MS IDs | Best MS/MS | AIF MS/MS ID |
|---|---|---|---|---|---|---|
| 148 | 716 | 10 | 12 | 226 | 226 | |
| 149 | 716 | 10 | 12 | 227;228 | 227 | |
| 153 | 716 | 10 | 14 | 233 | 233 | |
| 154 | 716 | 10 | 14 | 234 | 234 | |
| 155 | 716 | 11 | 15 | 235 | 235 | |
| 156 | 716 | 11 | 15 | 236 | 236 | |
| 157 | 716 | 11 | 16 | 237 | 237 | |
| 158 | 716 | 11 | 16 | 238 | 238 | |
| 910 | 197 | 91 | 106 | 1571 | 1571 | |
| 1035 | 1779 | 110 | 128 | 1731 | 1731 | |
| 1247 | 105 | 134 | 154 | 2088 | 2088 | |
| 3568 | 448 | 357 | 418 | 5939 | 5939 | |
| 3569 | 448 | 357 | 418 | 5940 | 5940 | |
| 3875 | 138 | 400 | 465 | 6370 | 6370 | |
| 4066 | 1087 | 423 | 492 | 6631 | 6631 | |
| 4067 | 1087 | 423 | 492 | 6632 | 6632 | |
| 4161 | 1429 | 438 | 507 | 6758 | 6758 | |
| 4265 | 1952 | 452 | 522 | 6917;6918;69 | 6917 | |
| 4266 | 1952 | 452 | 522 | 6920;6921 | 6921 | |
| 4267 | 1952 | 452 | 522 | 6922 | 6922 | |
| 4268 | 1952 | 452 | 522 | 6923 | 6923 | |
| 4269 | 1952 | 452 | 522 | 6924 | 6924 | |
| 4270 | 1952 | 452 | 522 | 6925 | 6925 | |
| 4271 | 1952 | 452 | 522 | 6926 | 6926 | |
| 4272 | 1952 | 452 | 522 | 6927 | 6927 | |
| 4273 | 1952 | 452 | 522 | | | |
| 4274 | 1952 | 452 | 522 | | | |
| 4275 | 1952 | 452 | 522 | | | |
| 4276 | 1952 | 452 | 523 | 6928 | 6928 | |
| 4390 | 719 | 465 | 537 | 7163 | 7163 | |
| 4694 | 109 | 494 | 576 | 7581 | 7581 | |
| 4695 | 109 | 494 | 576 | 7582 | 7582 | |
| 4696 | 109 | 494 | 576 | 7583 | 7583 | |
| 4697 | 109 | 494 | 576 | 7584 | 7584 | |
| 4698 | 109 | 494 | 576 | 7585 | 7585 | |
| 4699 | 109 | 494 | 576 | | | |
| 4704 | 109 | 494 | 578 | 7593;7594 | 7593 | |
| 4705 | 109 | 494 | 578 | 7595 | 7595 | |
| 5844 | 134 | 609 | 717 | 9553 | 9553 | |
| 5845 | 134 | 609 | 717 | 9554 | 9554 | |
| 5846 | 134 | 609 | 717 | 9555 | 9555 | |
| 5847 | 134 | 609 | 717 | 9556 | 9556 | |

| | | | | | |
|---|---|---|---|---|---|
| 5848 | 134 | 609 | 717 | 9557 | 9557 |
| 6080 | 285 | 636 | 748 | 9974 | 9974 |
| 6334 | 2177 | 658 | 776 | 10423;10424 | 10425 |
| 6335 | 2177 | 658 | 776 | 10426 | 10426 |
| 6336 | 2177 | 658 | 776 | | |
| 6506 | 1935 | 684 | 807 | 10663 | 10663 |
| 6807 | 1416 | 714 | 840 | 11241 | 11241 |
| 6808 | 1416 | 714 | 840 | 11242 | 11242 |
| 6839 | 1293 | 724 | 851 | 11286 | 11286 |
| 6840 | 1293 | 724 | 851 | 11287 | 11287 |
| 6841 | 1293 | 724 | 851 | 11288 | 11288 |
| 6906 | 147 | 734 | 861 | 11383 | 11383 |
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| 6912 | 147 | 734 | 861 | 11389 | 11389 |
| 6913 | 147 | 734 | 861 | 11390 | 11390 |
| 6914 | 147 | 734 | 861 | 11391 | 11391 |
| 6915 | 147 | 734 | 861 | 11392 | 11392 |
| 6916 | 147 | 734 | 861 | 11393;11394 | 11393 |
| 6917 | 147 | 734 | 861 | | |
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| 7098 | 969 | 757 | 886 | 11736;11737 | 11736 |
| 7099 | 969 | 757 | 886 | 11738 | 11738 |
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| 8884 | 298 | 969 | 1125 | 14594 | 14594 |
| 8925 | 625 | 976 | 1132 | 14655 | 14655 |
| 8926 | 625 | 976 | 1132 | | |
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| 11827 | 235 | 1310 | 1500 | 19705 | 19705 |
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| 13375 | 1621 | 1488 | 1708 | 22177 | 22177 |
| 14266 | 380 | 1578 | 1807 | 23676 | 23676 |

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| 14271 | 380 | 1578 | 1807 | 23681 | 23681 |
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| 15085 | 1598 | 1659 | 1899 | 25089 | 25089 |
| 15086 | 1598 | 1659 | 1899 | 25090 | 25090 |
| 15513 | 545 | 1708 | 1954 | 25813 | 25813 |
| 15548 | 939 | 1717 | 1964 | 25863 | 25863 |
| 15549 | 939 | 1717 | 1964 | 25864 | 25864 |
| 15550 | 939 | 1717 | 1964 | 25865 | 25865 |
| 16373 | 1256 | 1832 | 2095 | 27080 | 27080 |
| 17327 | 182 | 1946 | 2219 | 28791 | 28791 |
| 17699 | 1401 | 1997 | 2278 | 29358 | 29358 |
| 17922 | 1852 | 2030 | 2313 | 29690 | 29690 |
| 17923 | 1852 | 2030 | 2313 | 29691 | 29691 |
| 17924 | 1852 | 2030 | 2313 | 29692 | 29692 |
| 18364 | 816 | 2077 | 2363 | 30411 | 30411 |
| 18712 | 313 | 2121 | 2412 | 31012 | 31012 |
| 18726 | 1742 | 2125 | 2416 | 31035 | 31035 |
| 19350 | 707 | 2224 | 2527 | 31943 | 31943 |
| 19486 | 828 | 2258 | 2563 | 32110 | 32110 |
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| 19619 | 1091 | 2280 | 2586 | 32285 | 32285 |
| 19706 | 1013 | 2293 | 2601 | 32407 | 32407 |
| 19923 | 1041 | 2322 | 2634 | 32746 | 32746 |
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| 21457 | 1944 | 2500 | 2828 | 35299 | 35299 |
| 21458 | 1944 | 2500 | 2828 | 35300 | 35300 |
| 22352 | 1299 | 2614 | 2954 | 36806 | 36806 |
| 23072 | 1133 | 2706 | 3059 | 38116 | 38116 |
| 24199 | 87 | 2852 | 3215 | 39873 | 39873 |
| 24352 | 1907 | 2872 | 3235 | 40049 | 40049 |
| 24353 | 1907 | 2872 | 3235 | 40050 | 40050 |
| 24354 | 1907 | 2872 | 3235 | 40051 | 40051 |
| 25704 | 1465 | 3033 | 3411 | 42448 | 42448 |
| 26539 | 1728 | 3126 | 3521 | 43839 | 43839 |
| 26655 | 1034;1244 | 3144 | 3539 | 43998 | 43998 |
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| 32238 | 1968 | 3739 | 4198 | 53699 | 53699 |
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| 35505 | 404 | 4162 | 4669 | 59000 | 59000 |
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| 35661 | 498 | 4203 | 4712 | 59197 | 59197 |
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| 35810 | 731 | 4226 | 4736 | 59386 | 59386 |
| 35811 | 731 | 4226 | 4736 | 59387 | 59387 |
| 35812 | 731 | 4226 | 4736 | 59388 | 59388 |
| 35813 | 731 | 4226 | 4737 | 59389 | 59389 |
| 35854 | 1629 | 4229 | 4741 | 59439 | 59439 |
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| 36280 | 1930 | 4272 | 4789 | 60191 | 60191 |
| 36281 | 1690 | 4273 | 4790 | 60192 | 60192 |
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| 38655 | 2038 | 4618 | 5163 | 63836 | 63836 |
| 38952 | 2152 | 4663 | 5210 | 64260 | 64260 |
| 39294 | 310 | 4709 | 5258 | 64788 | 64788 |
| 40225 | 1748 | 4842 | 5404 | 66179 | 66179 |
| 41271 | 1503 | 4973 | 5548 | 67662 | 67662 |
| 42814 | 1816 | 5128 | 5724 | 70468 | 70468 |
| 42996 | 614 | 5149 | 5745 | 70795 | 70795 |
| 43473 | 1220 | 5225 | 5830 | 71572 | 71572 |
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| 43649 | 1561 | 5261 | 5868 | 71871 | 71871 |
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| 46028 | 548 | 5543 | 6192 | 75781 | 75781 |
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| 46057 | 1121 | 5554 | 6204 | 75815 | 75815 |
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| 46361 | 1989 | 5584 | 6246 | 76287 | 76287 |
| 46549 | 647 | 5608 | 6278 | 76621 | 76621 |
| 46550 | 647 | 5608 | 6278 | | |
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| 46891 | 191 | 5636 | 6321 | 77218 | 77218 |
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| 47031 | 1118 | 5661 | 6350 | 77453 | 77453 |
| 47032 | 1118 | 5661 | 6350 | 77454 | 77454 |
| 47033 | 1118 | 5661 | 6350 | 77455 | 77455 |
| 47121 | 125 | 5684 | 6376 | 77584 | 77584 |
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| 47123 | 416 | 5686 | 6378 | 77586 | 77586 |
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| 47547 | 2083 | 5716 | 6424 | 78326 | 78326 |
| 47557 | 1254 | 5721 | 6429 | 78343 | 78343 |
| 47582 | 1544 | 5726 | 6435 | 78378 | 78378 |
| 47583 | 507 | 5727 | 6436 | 78379 | 78379 |
| 47596 | 16 | 5731 | 6441 | 78393;78394 | 78394 |
| 47613 | 1584 | 5735 | 6445 | 78411 | 78411 |
| 47674 | 411 | 5744 | 6455 | 78499 | 78499 |
| 47675 | 411 | 5744 | 6455 | 78500 | 78500 |
| 47676 | 411 | 5744 | 6455 | 78501 | 78501 |
| 47727 | 491 | 5760 | 6472 | 78568 | 78568 |
| 47728 | 491 | 5760 | 6472 | 78569 | 78569 |
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| 47902 | 2032 | 5787 | 6503 | 78820 | 78820 |
| 48968 | 1501;867 | 5921 | 6666 | 80493 | 80493 |
| 49670 | 486 | 5987 | 6752 | 81753 | 81753 |
| 49724 | 1223 | 5991 | 6757 | 81840 | 81840 |
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| 49990 | 2155 | 6024 | 6792 | 82164 | 82164 |
| 50445 | 1481 | 6079 | 6855 | 83030 | 83030 |
| 51389 | 1283 | 6184 | 6978 | 84749 | 84749 |
| 51390 | 1283 | 6184 | 6978 | | |
| 51750 | 1339 | 6224 | 7022 | 85313 | 85313 |
| 51751 | 1339 | 6224 | 7022 | 85314 | 85314 |
| 51752 | 1339 | 6224 | 7022 | 85315 | 85315 |
| 52017 | 1085 | 6273 | 7073 | 85719 | 85719 |
| 52583 | 588 | 6321 | 7127 | 86615 | 86615 |
| 52584 | 588 | 6321 | 7128 | 86616 | 86616 |
| 53058 | 218 | 6387 | 7203 | 87380 | 87380 |
| 53073 | 588 | 6393 | 7209 | 87399 | 87399 |
| 53074 | 588 | 6393 | 7209 | 87400 | 87400 |
| 53293 | 148 | 6442 | 7263 | 87712 | 87712 |
| 54268 | 351 | 6571 | 7442 | 89157;89158 | 89158 |

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| 54270 | 351 | 6571 | 7443 | 89160 | 89160 |
| 55033 | 1116 | 6646 | 7552 | 90450 | 90450 |
| 55306 | 42 | 6674 | 7597 | 90807 | 90807 |
| 55307 | 42 | 6674 | 7597 | 90808 | 90808 |
| 55308 | 42 | 6674 | 7597 | 90809 | 90809 |
| 55309 | 42 | 6674 | 7597 | 90810 | 90810 |
| 55310 | 42 | 6674 | 7597 | 90811 | 90811 |
| 55311 | 42 | 6674 | 7597 | 90812 | 90812 |
| 55312 | 42 | 6674 | 7597 | 90813 | 90813 |
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| 55316 | 42 | 6674 | 7597 | 90817 | 90817 |
| 55317 | 42 | 6674 | 7597 | 90818 | 90818 |
| 55318 | 42 | 6674 | 7597 | 90819 | 90819 |
| 55319 | 42 | 6674 | 7597 | 90820 | 90820 |
| 55320 | 42 | 6674 | 7597 | 90821;90822 | 90821 |
| 55321 | 42 | 6674 | 7597 | 90823 | 90823 |
| 55322 | 42 | 6674 | 7597 | 90824 | 90824 |
| 55323 | 42 | 6674 | 7597 | 90825 | 90825 |
| 55412 | 280 | 6677 | 7604 | 90933 | 90933 |
| 55413 | 280 | 6677 | 7604 | 90934;90935 | 90934 |
| 55420 | 280 | 6678 | 7606 | 90941 | 90941 |
| 55421 | 280 | 6678 | 7606 | | |
| 55456 | 2023 | 6682 | 7611 | 91009 | 91009 |
| 55475 | 207 | 6688 | 7618 | 91039 | 91039 |
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| 56150 | 15 | 6767 | 7726 | 92066 | 92066 |
| 56151 | 15 | 6767 | 7726 | 92067 | 92067 |
| 56199 | 179 | 6773 | 7736 | 92131;92132 | 92131 |
| 56360 | 371 | 6794 | 7768 | 92357 | 92357 |
| 56475 | 242 | 6804 | 7786 | 92544 | 92544 |
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| 57058 | 586 | 6876 | 7887 | 93502 | 93502 |
| 57155 | 439 | 6895 | 7911 | 93618 | 93618 |
| 57291 | 896 | 6903 | 7927 | 93912 | 93912 |
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| 57336 | 1374 | 6907 | 7934 | | |
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| 58034 | 2183 | 6973 | 8040 | | |
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| 58607 | 1959 | 7058 | 8144 | 95986;95987 | 95987 |
| 58608 | 1959 | 7058 | 8144 | 95988 | 95988 |
| 58750 | 2050 | 7087 | 8173 | 96215 | 96215 |
| 58751 | 2050 | 7087 | 8173 | 96216 | 96216 |
| 58752 | 2050 | 7087 | 8173 | 96217 | 96217 |
| 58799 | 73 | 7093 | 8180 | 96270 | 96270 |
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| 58801 | 73 | 7093 | 8180 | | |
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| 60064 | 1276;1814;13 | 7314 | 8414 | 98101;98102 | 98102 |
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| 60165 | 1491 | 7320 | 8421 | 98309;98310 | 98309 |
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| 60167 | 1491 | 7320 | 8421 | 98313;98314 | 98313 |
| 60168 | 1491 | 7320 | 8421 | 98316 | 98316 |
| 60169 | 1491 | 7320 | 8421 | 98317;98318 | 98317 |
| 60170 | 1491 | 7320 | 8421 | 98319;98320 | 98321 |
| 60171 | 1491 | 7320 | 8421 | 98322 | 98322 |
| 60172 | 1491 | 7320 | 8421 | 98323;98324 | 98323 |
| 60173 | 1491 | 7320 | 8421 | 98327;98328 | 98329 |
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| 60176 | 1491 | 7320 | 8421 | 98336;98337 | 98341 |
| 60177 | 1491 | 7320 | 8421 | 98345 | 98345 |
| 60178 | 1491 | 7320 | 8421 | 98346 | 98346 |
| 60179 | 1491 | 7320 | 8421 | 98347;98348 | 98349 |
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| 60182 | 1491 | 7320 | 8421 | 98357 | 98357 |
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| 63048 | 2046 | 7660 | 8804 | 103205;1032 | 103206 |
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| 63051 | 1324 | 7661 | 8806 | | |
| 63073 | 163 | 7666 | 8811 | 103230 | 103230 |
| 63074 | 163 | 7666 | 8812 | 103231 | 103231 |
| 63075 | 163 | 7666 | 8812 | | |
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| 64173 | 2116 | 7792 | 8950 | 104879 | 104879 |
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| 64682 | 16 | 7867 | 9030 | 105619;1056 | 105620 |
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| 64684 | 16 | 7867 | 9030 | 105622 | 105622 |

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| 64686 | 16 | 7867 | 9031 | 105624 | 105624 |
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| 65090 | 1089 | 7929 | 9097 | 106297 | 106297 |
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| 65363 | 700 | 7977 | 9150 | 106669 | 106669 |
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| 66336 | 1008 | 8094 | 9282 | 108310;1083 | 108311 |
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| 69221 | 480 | 8379 | 9598 | 113381 | 113381 |
| 69542 | 1481 | 8405 | 9630 | 114045 | 114045 |
| 70014 | 241 | 8457 | 9686 | 115037 | 115037 |
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| 70611 | 1073 | 8523 | 9763 | 116065 | 116065 |
| 71295 | 1756 | 8615 | 9866 | 117351 | 117351 |
| 71481 | 317 | 8639 | 9894 | 117739 | 117739 |
| 71538 | 2101 | 8646 | 9902 | 117814 | 117814 |
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| 72615 | 1988 | 8751 | 10018 | 119612 | 119612 |
| 74264 | 434 | 8922 | 10209 | 122344 | 122344 |
| 74265 | 434 | 8922 | 10209 | 122345;1223 | 122346 |
| 74266 | 434 | 8922 | 10209 | 122347 | 122347 |
| 77619 | 925 | 9284 | 10621 | 127839;1278 | 127839 |
| 77620 | 925 | 9284 | 10621 | 127841 | 127841 |
| 77621 | 925 | 9284 | 10621 | 127842;1278 | 127843 |
| 78230 | 38 | 9354 | 10698 | 128761 | 128761 |
| 79136 | 1801 | 9454 | 10810 | 130187 | 130187 |
| 79137 | 1801 | 9454 | 10810 | 130188 | 130188 |
| 79325 | 1455 | 9468 | 10826 | 130479 | 130479 |
| 79326 | 1455 | 9468 | 10826 | 130480 | 130480 |
| 79327 | 1455 | 9468 | 10826 | 130481 | 130481 |
| 79339 | 1483 | 9471 | 10829 | 130496 | 130496 |
| 79529 | 331 | 9487 | 10848 | 130771 | 130771 |
| 79541 | 1066 | 9490 | 10851 | 130784 | 130784 |
| 79542 | 1066 | 9490 | 10851 | | |
| 79957 | 51 | 9524 | 10888 | 131513 | 131513 |
| 80825 | 788 | 9608 | 10982 | 132956 | 132956 |
| 80826 | 788 | 9608 | 10982 | 132957 | 132957 |

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| 81631 | 415 | 9725 | 11109 | 134163 | 134163 |
| 82115 | 496 | 9792 | 11181 | 134919 | 134919 |
| 82116 | 496 | 9792 | 11181 | 134920 | 134920 |
| 82130 | 1665 | 9796 | 11185 | 134947 | 134947 |
| 82131 | 1665 | 9796 | 11185 | | |
| 82248 | 1756 | 9817 | 11207 | 135143 | 135143 |
| 82327 | 1540 | 9830 | 11220 | 135244 | 135244 |
| 82455 | 566 | 9846 | 11238 | 135431 | 135431 |
| 82568 | 1908 | 9861 | 11255 | 135596 | 135596 |
| 82981 | 1252 | 9898 | 11300 | 136397 | 136397 |
| 83162 | 1869 | 9914 | 11318 | 136763 | 136763 |
| 83216 | 269 | 9920 | 11324 | 136833 | 136833 |

| Deamidation | Oxidation (M | Phospho (STY) site IDs |
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| Sequence | Length | K Count | Modifications | Modified sequence | Deamidation (NQ) Probabilities | Oxidation (M) Probabilities |
|---|---|---|---|---|---|---|
| AAAPAAVASP | 25 | 1 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 25 | 1 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 25 | 1 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAK_ | | |
| AAAPAAVASP | 25 | 1 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAK_ | | |
| AAAPAAVASP | 26 | 2 | Phospho (STY | _AAAPAAVASPAAAATS(ph)ADASPSPAKK_ | | |
| AAAPAAVASP | 26 | 2 | Phospho (STY | _AAAPAAVASPAAAATSADASPS(ph)PAKK_ | | |
| AAAPAAVASP | 26 | 2 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADASPS(ph)PA | | |
| AAAPAAVASP | 26 | 2 | 2 Phospho (S | _AAAPAAVAS(ph)PAAAATSADAS(ph)PSPA | | |
| | | | | | | |
| ALDLLMSYRLI | 11 | 1 | Oxidation (M | _ALDLLM(ox)S(ph)Y(ph)RLK | ALDLLM(1)SY | |
| ALDLLMSYRLI | 11 | 1 | Oxidation (M | _ALDLLM(ox)S(ph)Y(ph)RLK | ALDLLM(1)SY | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLTAS(ph)HNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(ph)ASHNPGGPENDFGIK_ | | |
| ALGGIVLTASH | 23 | 1 | Phospho (STY | _ALGGIVLT(p | ALGGIVLTASHN(0.529)PGG | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | Phospho (STY | _ALQAVYPDYVDELSLYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | 2 Phospho (S | _ALQAVYPDYVDELS(ph)LYGS(ph)K_ | | |
| ALQAVYPDYV | 19 | 1 | 2 Phospho (S | _ALQAVYPDYVDELS(ph)LYGS(ph)K_ | | |
| | | | | | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |
| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD | | |

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| APATPQAATS | 39 | 2 | Phospho (STY | _APATPQAATSVTNPAAGDGISVQNDPPVD |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| ASAFQFSDDE | 14 | 1 | Phospho (STY | _ASAFQFS(ph)DDEEEVK_ |
| | | | | |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)ASGVT(ph)VSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)AS(ph)GVTVSDVCK_ |
| ASGVTVSDVC | 11 | 1 | Acetyl (Protei | _(ac)ASGVT(ph)VSDVCK_ |
| DLEYFNNLK | 9 | 1 | Phospho (STY | _DLEY(ph)FN( | DLEYFN(1)N(1)LK |
| DLEYFNNLK | 9 | 1 | Phospho (STY | _DLEY(ph)FN( | DLEYFN(1)N(1)LK |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| DVDFGDSDNI | 21 | 1 | Phospho (STY | _DVDFGDS(ph)DNENEPDAYLARLK_ |
| EAAQYGTVNA | 14 | 1 | Phospho (STY | _EAAQY(ph)GTVNAVLPK_ |
| EAAQYGTVNA | 14 | 1 | Phospho (STY | _EAAQY(ph)GTVNAVLPK_ |
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVSM(ox)AS(ph)PAKD | EASPVSM(1)A |

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|---|---|---|---|---|---|
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVSM(ox)AS(ph)PAKD | EASPVSM(1)A |
| EASPVSMASP | 25 | 2 | Oxidation (M | _EASPVS(ph)M(ox)ASPAKD | EASPVSM(1)A |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | |
| ELPDSDSLNV/ | 27 | 1 | Phospho (STY | _ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_ | |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( |
| FFDSGDYQM/ | 11 | 1 | Oxidation (M | _FFDS(ph)GDYQM(ox)AK_ | FFDSGDYQM( |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF/ | KEESESEDDDI |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF/ | KEESESEDDDI |
| KEESESEDDDI | 17 | 1 | Oxidation (M | _KEESES(ph)EDDDM(ox)GF/ | KEESESEDDDI |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPESSAKVS(ph)DAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KIDNPESSAKV | 25 | 3 | Phospho (STY | _KIDNPES(ph)SAKVSDAEEEEEEYAVEK_ | |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEES(ph)DQS(ph)DDDM | KKEEESDQSD |
| KKEEESDQSD | 19 | 2 | Oxidation (M | _KKEEESDQS(ph)DDDM(ox) | KKEEESDQSD |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| KPEDPSSEAE/ | 17 | 2 | Phospho (STY | _KPEDPSSEAEALCS(ph)PAK_ | |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | M(1)PNLQSSI |
| MPNLQSSIPH | 13 | 2 | Acetyl (Protei | _(ac)M(ox)PNLQS(ph)SIPHT | M(1)PNLQSSI |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILS( | MQ(0.212)LILSYLQ(0.848)S( |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY | MQ(0.007)LILSYLQ(0.996)S( |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_ | |
| MQLILSYLQSC | 14 | 1 | Acetyl (Protei | _(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_ | |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)Q(de)I | MQ(0.844)LIL M(1)QLILSYLC |

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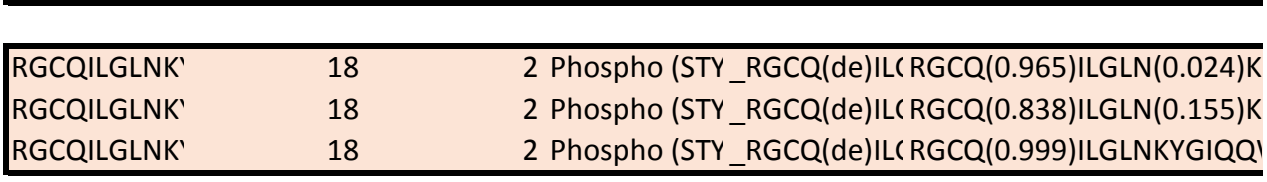
|---|---|---|---|---|---|
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)QLILSY | MQ(0.066)LIL M(1)QLILSYLC |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_ | |
| MQLILSYLQSC | 14 | 1 | Oxidation (M | _M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_ | |
| | | | | | |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.0 M(1)RDKISQL |
| MRDKISQLFC | 13 | 2 | Acetyl (Protei | _(ac)M(ox)RD | MRDKISQ(0.2 M(1)RDKISQL |
| | | | | | |
| MVEPSPETVC | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | M(1)VEPSPET |
| MVEPSPETVC | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | M(1)VEPSPET |
| MVEPSPETVC | 24 | 1 | Oxidation (M | _M(ox)VEPSPETVGDFQSVQ | M(1)VEPSPET |
| | | | | | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | |
| NAGGVGVGV | 17 | 2 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLK_ | |
| NAGGVGVGV | 18 | 3 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLKK_ | |
| NAGGVGVGV | 18 | 3 | Phospho (STY | _NAGGVGVGVGEKS(ph)PDLKK_ | |
| | | | | | |
| NVGIFIKDDSL | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | |
| NVGIFIKDDSL | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | |
| NVGIFIKDDSL | 19 | 3 | Phospho (STY | _NVGIFIKDDS(ph)DEEDVDDKK_ | |
| | | | | | |
| PCNLYQTAQE | 13 | 1 | Phospho (STY | _PCNLY(ph)QTAQEQLK_ | |
| PCNLYQTAQE | 13 | 1 | Phospho (STY | _PCN(de)LY(p | PCN(0.992)LYQ(0.004)TAQ( |
| | | | | | |
| PLPSGRIPQITI | 17 | 1 | 2 Phospho (S | _PLPS(ph)GRIPQIT(ph)PPASPK_ | |
| PLPSGRIPQITI | 17 | 1 | 2 Phospho (S | _PLPS(ph)GRIPQIT(ph)PPASPK_ | |
| | | | | | |
| QELLQSYMK | 9 | 1 | Oxidation (M | _(gl)Q(de)ELL | Q(1)ELLQ(1)S QELLQSYM(1) |
| QELLQSYMK | 9 | 1 | Oxidation (M | _(gl)Q(de)ELL | Q(1)ELLQ(1)S QELLQSYM(1) |
| QELLQSYMK | 9 | 1 | Phospho (STY | _(gl)Q(de)ELL | Q(1)ELLQ(1)SYMK |
| | | | | | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |
| QISIGIYELLK | 11 | 1 | Phospho (STY | _QISIGIY(ph)ELLK_ | |

| | | | |
|---|---|---|---|
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| QISIGIYELLK | 11 | 1 | Phospho (STY _QISIGIY(ph)ELLK_ |
| | | | |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| QSSYHGVHQ/ | 18 | 1 | Phospho (STY _(gl)QSSYHGVHQAWNTNQDS(ph)K_ |
| | | | |
| QSVPQLANLT | 16 | 1 | Phospho (STY _Q(de)SVPQ( |
| QSVPQLANLT | 16 | 1 | Phospho (STY _Q(de)SVPQ( |
| QSVPQLANLT | 16 | 1 | Phospho (STY _Q(de)SVPQ( |
| QSVPQLANLT | 16 | 1 | Phospho (STY _Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_ |
| QSVPQLANLT | 16 | 1 | Phospho (STY _Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_ |
| | | | |
| REEENAAAAE | 31 | 1 | Phospho (STY _REEENAAAAEEEAGEISATGGATS(ph)PEP |
| REEENAAAAE | 31 | 1 | Phospho (STY _REEENAAAAEEEAGEISATGGAT(ph)SPEP |
| REEENAAAAE | 31 | 1 | Phospho (STY _REEENAAAAEEEAGEISATGGAT(ph)SPEP |
| | | | |
| RGCQILGLNK | 18 | 2 | Phospho (STY _RGCQ(de)IL( |
| RGCQILGLNK | 18 | 2 | Phospho (STY _RGCQ(de)IL( |
| RGCQILGLNK | 18 | 2 | Phospho (STY _RGCQ(de)IL( |
| | | | |
| RGPPPPPTAS | 17 | 1 2 | Phospho (S _RGPPPPPTA |
| RGPPPPPTAS | 17 | 1 2 | Phospho (S _RGPPPPPTASES(ph)T(ph)RRN(de)K_ |
| RGPPPPPTAS | 17 | 1 2 | Phospho (S _RGPPPPPTASES(ph)T(ph)RRN(de)K_ |
| | | | |
| RKKPEDPSSE/ | 19 | 3 | Phospho (STY _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | 3 | Phospho (STY _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSE/ | 19 | 3 | Phospho (STY _RKKPEDPSSEAEALCS(ph)PAK_ |



| | | | | |
|---|---|---|---|---|
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |
| RKKPEDPSSEA | 19 | 3 | Phospho (STY | _RKKPEDPSSEAEALCS(ph)PAK_ |

| | | | | |
|---|---|---|---|---|
| SAAVAEGGDA | 23 | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGDA | 23 | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGDA | 23 | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGDA | 23 | 2 | Phospho (STY | _SAAVAEGGDAVAET(ph)AKGEEGSPK_ |
| SAAVAEGGDA | 23 | 2 | Phospho (STY | _SAAVAEGGDAVAETAKGEEGS(ph)PK_ |

| | | | | |
|---|---|---|---|---|
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVS(ph)SPSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVS(ph)SPSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSSPS(ph)K_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |
| SAEAEAIVTTA | 20 | 1 | Acetyl (Protei | _(ac)SAEAEAIVTTATADVSS(ph)PSK_ |

| | | | | |
|---|---|---|---|---|
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVAT(ph)SASPVAAPPATVEK_ |

| | | | | |
|---|---|---|---|---|
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVATS(ph)ASPVAAPPATVEK_ |
| SDSAVATSASI | 21 | 1 | Acetyl (Protei | _(ac)SDSAVAT(ph)SASPVAAPPATVEK_ |
| | | | | |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPSI | 14 | 1 | Phospho (STY | _SPIVFELTQPS(ph)PEK_ |
| SPIVFELTQPSI | 14 | 1 | 2 Phospho (S | _S(ph)PIVFELTQPS(ph)PEK_ |
| | | | | |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| SVHSPNPGLIL | 14 | 1 | Acetyl (Protei | _(ac)SVHS(ph)PNPGLILQSK_ |
| | | | | |
| TSPKPTKPASF | 12 | 3 | Phospho (STY | _TSPKPTKPAS(ph)PK_ |
| TSPKPTKPASF | 12 | 3 | Phospho (STY | _TSPKPTKPAS(ph)PK_ |
| | | | | |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| VDRSDNAAES | 25 | 1 | Acetyl (Protei | _(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI |
| | | | | |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEH |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEH |
| VNSLIVLESDE | 33 | 1 | Phospho (STY | _VNSLIVLES(ph)DEEEDEQLVQAADLVEQEH |
| | | | | |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIVC | VTILWM(1)GC |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIVC | VTILWM(1)GC |
| VTILWMGGSC | 19 | 1 | Oxidation (M | _VT(ph)ILWM(ox)GGSGSIVC | VTILWM(1)GC |

| Phospho (STY) Probabilities | Deamidation (NQ) Score Diffs | Oxidation (M) Score Diffs | Phospho (STY) Score Diffs | Acetyl (Protein N-term) | Deamidation (NQ) | Gln->pyro-Glu |
|---|---|---|---|---|---|---|
| AAAPAAVAS(0.997)PAAAAT(0.005)S(0.00 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.995)PAAAAT(0.003)S(0.00 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVASPAAAAT(0.005)S(0.034)ADAS | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVASPAAAAT(0.006)S(0.042)ADAS | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.078)PAAAAT(0.34)S(0.427 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.004)PAAAAT(0.062)S(0.28 | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.993)PAAAAT(0.03)S(0.03)A | | | AAAPAAVAS( | 0 | 0 | 0 |
| AAAPAAVAS(0.985)PAAAAT(0.077)S(0.08 | | | AAAPAAVAS( | 0 | 0 | 0 |
| | | | | | | |
| ALDLLMS(1)Y(1)RLK | | ALDLLM(45.4 | ALDLLMS(45. | 0 | 0 | 0 |
| ALDLLMS(1)Y(1)RLK | | ALDLLM(57.1 | ALDLLMS(57. | 0 | 0 | 0 |
| ALGGIVLT(0.066)AS(0.934)HNPGGPENDF | | | ALGGIVLT(-11 | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.784)AS(0.216)HNPGGPENDF | | | ALGGIVLT(5.6 | 0 | 0 | 0 |
| ALGGIVLT(0.121)AS(0.879)HNPGGPENDF | | | ALGGIVLT(-8. | 0 | 0 | 0 |
| ALGGIVLT(0.098)AS(0.902)HNPGGPENDF | | | ALGGIVLT(-9. | 0 | 0 | 0 |
| ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK | | | ALGGIVLT(0)A | 0 | 0 | 0 |
| ALGGIVLT(0.204)AS(0.796)HNPGGPENDF | | | ALGGIVLT(-5. | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| ALGGIVLT(0.5 | ALGGIVLTASHN(-0.65)PGGI | | ALGGIVLT(0.6 | 0 | 1 | 0 |
| ALQAVYPDYVDELS(0.161)LY(0.135)GS(0.7 | | | ALQAVY(-67.3 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.021)LY(0.015)GS(0.9 | | | ALQAVY(-63.3 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.001)LY(0.057)GS(0.9 | | | ALQAVY(-81.2 | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.001)LY(0.016)GS(0.9 | | | ALQAVY(-70.6 | 0 | 0 | 0 |
| ALQAVYPDY(0.002)VDELS(0.04)LY(0.004) | | | ALQAVY(-51.2 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| ALQAVYPDYVDELS(0.996)LY(0.009)GS(0.9 | | | ALQAVY(-75.9 | 0 | 0 | 0 |
| ALQAVY(0.084)PDY(0.078)VDELS(0.605)L | | | ALQAVY(-10.4 | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.001)VQNI | | | APAT(-56.02) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.001)VQNI | | | APAT(-50.33) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.002)VQNI | | | APAT(-39.76) | 0 | 0 | 0 |
| APATPQAATSVTNPAAGDGIS(0.004)VQNI | | | APAT(-40.05) | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| APATPQAATSVTNPAAGDGIS(0.004)VQNI | APAT(-44.28) | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-64.04)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-48.64)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-75.24)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-54.82)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-61.47)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-59.12)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-56.8)AFQ | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-42.65)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-66.2)AFQ | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-67.24)AF( | 0 | 0 | 0 |
| ASAFQFS(1)DDEEEVK | AS(-96.36)AF( | 0 | 0 | 0 |
| | | 0 | 0 | 0 |
| AS(1)GVTVSDVCK | AS(39.82)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | AS(38.57)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | AS(40.23)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | AS(38.02)GVT | 1 | 0 | 0 |
| AS(0.977)GVT(0.022)VSDVCK | AS(16.42)GVT | 1 | 0 | 0 |
| AS(0.997)GVT(0.003)VSDVCK | AS(25.59)GVT | 1 | 0 | 0 |
| AS(0.42)GVT(0.568)VS(0.012)DVCK | AS(-1.31)GVT | 1 | 0 | 0 |
| AS(0.998)GVT(0.002)VSDVCK | AS(26.02)GVT | 1 | 0 | 0 |
| AS(1)GVTVSDVCK | AS(35.02)GVT | 1 | 0 | 0 |
| AS(0.976)GVT(0.023)VS(0.001)DVCK | AS(16.37)GVT | 1 | 0 | 0 |
| | | 1 | 0 | 0 |
| DLEY(1)FNNL | DLEYFN(65.22)N(65.22)LK | DLEY(65.22)F | 0 | 2 | 0 |
| DLEY(1)FNNL | DLEYFN(54.07)N(54.07)LK | DLEY(54.07)F | 0 | 2 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | DVDFGDS(53. | 0 | 0 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | DVDFGDS(67. | 0 | 0 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | DVDFGDS(43. | 0 | 0 | 0 |
| DVDFGDS(1)DNENEPDAYLARLK | DVDFGDS(56. | 0 | 0 | 0 |
| DVDFGDS(0.994)DNENEPDAY(0.006)LARI | DVDFGDS(22. | 0 | 0 | 0 |
| DVDFGDS(0.999)DNENEPDAY(0.001)LARI | DVDFGDS(31. | 0 | 0 | 0 |
| EAAQY(0.933)GT(0.067)VNAVLPK | EAAQY(11.44 | 0 | 0 | 0 |
| EAAQY(0.799)GT(0.201)VNAVLPK | EAAQY(6)GT( | 0 | 0 | 0 |
| EAS(0.012)PVS(0.157)MAS( | EASPVSM(53. | EAS(-18.36)P | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| EAS(0.014)PVS(0.221)MAS( | EASPVSM(53. | EAS(-17.37)P | 0 | 0 | 0 |
| EAS(0.127)PVS(0.465)MAS( | EASPVSM(40. | EAS(-5.65)PV | 0 | 0 | 0 |
| ELPDSDSLNVAPPEGFS(1)DEEPEERQCK | | ELPDS(-46.35 | 0 | 0 | 0 |
| ELPDSDSLNVAPPEGFS(1)DEEPEERQCK | | ELPDS(-49.23 | 0 | 0 | 0 |
| ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEP | | ELPDS(-38.75 | 0 | 0 | 0 |
| FFDS(1)GDYQMAK | FFDSGDYQM( | FFDS(40.97)G | 0 | 0 | 0 |
| FFDS(0.994)GDY(0.006)QM | FFDSGDYQM( | FFDS(22.15)G | 0 | 0 | 0 |
| FFDS(1)GDYQMAK | FFDSGDYQM( | FFDS(36.09)G | 0 | 0 | 0 |
| KEES(0.181)ES(0.819)EDDD | KEESESEDDDI | KEES(-6.55)ES | 0 | 0 | 0 |
| KEES(0.209)ES(0.791)EDDD | KEESESEDDDI | KEES(-5.78)ES | 0 | 0 | 0 |
| KEES(0.074)ES(0.926)EDDD | KEESESEDDDI | KEES(-10.98)E | 0 | 0 | 0 |
| KIDNPES(0.333)S(0.333)AKVS(0.333)DAEI | | KIDNPES(0)S( | 0 | 0 | 0 |
| KIDNPES(0.012)S(0.022)AKVS(0.966)DAEI | | KIDNPES(-19. | 0 | 0 | 0 |
| KIDNPES(0.489)S(0.489)AKVS(0.022)DAEI | | KIDNPES(0)S( | 0 | 0 | 0 |
| KIDNPES(0.567)S(0.41)AKVS(0.023)DAEEI | | KIDNPES(1.41 | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | KKEEESDQSDI | KKEEES(46.14 | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | KKEEESDQSDI | KKEEES(46.7) | 0 | 0 | 0 |
| KKEEES(1)DQS(1)DDDMGFC | KKEEESDQSDI | KKEEES(42.09 | 0 | 0 | 0 |
| KKEEES(0.035)DQS(0.965)D | KKEEESDQSDI | KKEEES(-14.3 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-47.0 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-37.5 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-41.9 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-51.7 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-69.7 | 0 | 0 | 0 |
| KPEDPSSEAEALCS(1)PAK | | KPEDPS(-49.5 | 0 | 0 | 0 |
| MPNLQS(0.857)S(0.121)IPH | M(56.2)PNLQ | MPNLQS(8.49 | 1 | 0 | 0 |
| MPNLQS(0.492)S(0.492)IPH | M(40.24)PNL( | MPNLQS(0)S( | 1 | 0 | 0 |
| MPNLQS(0.778)S(0.175)IPH | M(47.71)PNL( | MPNLQS(6.47 | 1 | 0 | 0 |
| MPNLQS(0.497)S(0.497)IPH | M(58.89)PNL( | MPNLQS(0)S( | 1 | 0 | 0 |
| MQLILS(0.695 | MQ(-7.66)LILSYLQ(7.66)SQ( | MQLILS(7.66) | 1 | 3 | 0 |
| MQLILS(0.245 | MQ(-25.8)LILSYLQ(25.8)SQ( | MQLILS(-4.01 | 1 | 3 | 0 |
| | | | 1 | 3 | 0 |
| | | | 1 | 3 | 0 |
| MQLILS(0.974 | MQ(7.74)LILS | M(44.25)QLIL | MQLILS(19.37 | 0 | 2 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| MQLILS(0.201 | MQ(-13.61)LI | M(43.69)QLIL | MQLILS(-5.35 | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| | | | | 0 | 2 | 0 |
| MRDKIS(1)QL | MRDKISQ(-15 | M(62.09)RDK | MRDKIS(62.0 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-15 | M(54.34)RDK | MRDKIS(54.3 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-10 | M(56.2)RDKI | MRDKIS(56.2 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-17 | M(51.13)RDK | MRDKIS(51.1 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-12 | M(51.46)RDK | MRDKIS(51.4 | 1 | 1 | 0 |
| MRDKIS(1)QL | MRDKISQ(-4.4 | M(43.8)RDKI | MRDKIS(43.8 | 1 | 1 | 0 |
| MVEPSPETVGDFQSVQEEVE | | M(86.56)VEP | MVEPS(-69.6 | 0 | 0 | 0 |
| MVEPSPETVGDFQS(0.245)\ | | M(50.26)VEP | MVEPS(-41.7 | 0 | 0 | 0 |
| MVEPSPETVGDFQS(0.001)\ | | M(50.32)VEP | MVEPS(-37.1 | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | NAGGVGVGV | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | NAGGVGVGV | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | NAGGVGVGV | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLK | | NAGGVGVGV | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLKK | | NAGGVGVGV | | 0 | 0 | 0 |
| NAGGVGVGVGEKS(1)PDLKK | | NAGGVGVGV | | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | NVGIFIKDDS( | | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | NVGIFIKDDS( | | 0 | 0 | 0 |
| NVGIFIKDDS(1)DEEDVDDKK | | NVGIFIKDDS( | | 0 | 0 | 0 |
| PCNLY(0.854)QT(0.146)AQEQLK | | PCNLY(7.67)C | | 0 | 0 | 0 |
| PCNLY(0.962) | PCN(24.93)LYQ(-24.93)TAQ | PCNLY(14.07) | | 0 | 1 | 0 |
| PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK | | PLPS(41.55)G | | 0 | 0 | 0 |
| PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK | | PLPS(33.2)GR | | 0 | 0 | 0 |
| QELLQS(0.87 | Q(51.95)ELLC | QELLQSYM(5 | QELLQS(8.31) | 0 | 2 | 1 |
| QELLQS(0.84 | Q(41.43)ELLC | QELLQSYM(4 | QELLQS(7.5)Y | 0 | 2 | 1 |
| QELLQS(0.24 | Q(45.02)ELLQ | (45.02)SYMK | QELLQS(-4.96 | 0 | 2 | 1 |
| QISIGIY(1)ELLK | | | QIS(-47.73)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-48.31)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-46.94)IG | 0 | 0 | 0 |
| QIS(0.001)IGIY(0.999)ELLK | | | QIS(-32.34)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-55.01)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | | | QIS(-38.47)IG | 0 | 0 | 0 |

| | | | | |
|---|---|---|---|---|
| QISIGIY(1)ELLK | QIS(-43.94)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-39.86)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-57.55)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-35.76)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-50.69)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-47.93)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-49.83)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-53)IGIY(S | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-39.44)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-55.72)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-52.88)IG | 0 | 0 | 0 |
| QISIGIY(1)ELLK | QIS(-36.23)IG | 0 | 0 | 0 |

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|---|---|---|---|---|
| QSSYHGVHQAWNT(0.042)NQDS(0.957)K | QS(-41.5)S(-4 | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.028)NQDS(0.972)K | QS(-47.65)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.042)NQDS(0.958)K | QS(-80.23)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.001)NQDS(0.999)K | QS(-87.48)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.01)NQDS(0.99)K | QS(-52.27)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.025)NQDS(0.975)K | QS(-60.4)S(-6 | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.005)NQDS(0.995)K | QS(-73.94)S(- | 0 | 0 | 1 |
| QSSYHGVHQAWNT(0.128)NQDS(0.872)K | QS(-48.42)S(- | 0 | 0 | 1 |

| | | | | |
|---|---|---|---|---|
| QS(0.014)VPC | Q(21.8)SVPQ(21.8)LAN(20.: | QS(-21.8)VPC | 0 | 3 | 0 |
| QS(0.005)VPC | Q(13.41)SVPQ(14.75)LAN(5 | QS(-25.08)VP | 0 | 3 | 0 |
| QS(0.006)VPC | Q(11.59)SVPQ(18.04)LAN(6 | QS(-24.64)VP | 0 | 3 | 0 |
| | | | 0 | 3 | 0 |
| | | | 0 | 3 | 0 |

| | | | | |
|---|---|---|---|---|
| REEENAAAAEEEAGEISAT(0.01)GGAT(0.21 | REEENAAAAE | 0 | 0 | 0 |
| REEENAAAAEEEAGEISAT(0.001)GGAT(0.4 | REEENAAAAE | 0 | 0 | 0 |
| REEENAAAAEEEAGEIS(0.005)AT(0.02)GG/ | REEENAAAAE | 0 | 0 | 0 |

| | | | | |
|---|---|---|---|---|
| RGCQILGLNK' | RGCQ(16.13)ILGLN(-16.13)I | RGCQILGLNK' | 0 | 1 | 0 |
| RGCQILGLNK' | RGCQ(7.33)ILGLN(-7.33)KY( | RGCQILGLNK' | 0 | 1 | 0 |
| RGCQILGLNK' | RGCQ(33.24)ILGLN(-33.24)I | RGCQILGLNK' | 0 | 1 | 0 |

| | | | | |
|---|---|---|---|---|
| RGPPPPPT(0.( | RGPPPPPTASESTRRN(43.11 | RGPPPPPT(-2 | 0 | 1 | 0 |
| | | | 0 | 1 | 0 |
| | | | 0 | 1 | 0 |

| | | | | |
|---|---|---|---|---|
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-5( | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4- | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4: | 0 | 0 | 0 |

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|---|---|---|---|---|
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-3 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-3 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-4 | 0 | 0 | 0 |
| RKKPEDPSSEAEALCS(1)PAK | RKKPEDPS(-5 | 0 | 0 | 0 |

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|---|---|---|---|---|
| SAAVAEGGDAVAET(0.733)AKGEEGS(0.26 | S(-42.23)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.901)AKGEEGS(0.09 | S(-58.47)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.614)AKGEEGS(0.38 | S(-39.38)AAV | 0 | 0 | 0 |
| S(0.001)AAVAEGGDAVAET(0.702)AKGEE( | S(-28.94)AAV | 0 | 0 | 0 |
| SAAVAEGGDAVAET(0.209)AKGEEGS(0.79 | S(-48.44)AAV | 0 | 0 | 0 |

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|---|---|---|---|---|
| SAEAEAIVTTATADVS(0.307)S(0.514)PS(0. | S(-107.65)AE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.034)S(0.483)PS(0. | S(-78.78)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.051)S(0.77)PS(0.1 | S(-102.74)AE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.007)S(0.496)PS(0. | S(-76.49)AEA | 1 | 0 | 0 |
| SAEAEAIVT(0.022)T(0.02)AT(0.067)ADVS( | S(-61.37)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.01)S(0.495)PS(0.4 | S(-54.67)AEA | 1 | 0 | 0 |
| SAEAEAIVTT(0.001)AT(0.004)ADVS(0.046 | S(-61.79)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.019)S(0.957)PS(0. | S(-108.85)AE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.041)S(0.479)PS(0. | S(-81.76)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.047)S(0.743)PS(0. | S(-102.8)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.48)S(0.329)PS(0.1 | S(-50.28)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.045)S(0.421)PS(0. | S(-119.63)AE | 1 | 0 | 0 |
| SAEAEAIVTTAT(0.001)ADVS(0.035)S(0.37 | S(-66.49)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.007)S(0.783)PS(0. | S(-112.12)AE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.052)S(0.762)PS(0. | S(-82.71)AEA | 1 | 0 | 0 |
| SAEAEAIVT(0.01)T(0.012)AT(0.04)ADVS(0 | S(-39.1)AEAE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.067)S(0.467)PS(0. | S(-77.93)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.021)S(0.489)PS(0. | S(-77.91)AEA | 1 | 0 | 0 |
| SAEAEAIVTT(0.002)AT(0.006)ADVS(0.174 | S(-40.69)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.035)S(0.71)PS(0.2 | S(-81.87)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.175)S(0.771)PS(0. | S(-108.29)AE | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.035)S(0.813)PS(0. | S(-91.77)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.008)S(0.158)PS(0. | S(-76.74)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.066)S(0.717)PS(0. | S(-108.3)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.185)S(0.408)PS(0. | S(-80.53)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.018)S(0.396)PS(0. | S(-55.82)AEA | 1 | 0 | 0 |
| SAEAEAIVTTATADVS(0.068)S(0.878)PS(0. | S(-89.55)AEA | 1 | 0 | 0 |
| | | 1 | 0 | 0 |

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|---|---|---|---|---|
| S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS( | S(-16.63)DS(- | 1 | 0 | 0 |

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|---|---|---|---|---|
| S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0 | S(-18.26)DS(- | 1 | 0 | 0 |
| SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP | S(-34.71)DS(- | 1 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-54.97)PIVF | 0 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-67.16)PIVF | 0 | 0 | 0 |
| SPIVFELT(0.001)QPS(0.999)PEK | S(-63.62)PIVF | 0 | 0 | 0 |
| SPIVFELTQPS(1)PEK | S(-86.11)PIVF | 0 | 0 | 0 |
| SPIVFELTQPS(1)PEK | S(-70.03)PIVF | 0 | 0 | 0 |
| S(1)PIVFELT(0.009)QPS(0.991)PEK | S(40.41)PIVFE | 0 | 0 | 0 |
| S(0.06)VHS(0.94)PNPGLILQSK | S(-11.98)VHS( | 1 | 0 | 0 |
| S(0.003)VHS(0.997)PNPGLILQSK | S(-25.47)VHS( | 1 | 0 | 0 |
| S(0.002)VHS(0.998)PNPGLILQSK | S(-27.48)VHS( | 1 | 0 | 0 |
| S(0.008)VHS(0.992)PNPGLILQSK | S(-21.15)VHS( | 1 | 0 | 0 |
| TSPKPT(0.028)KPAS(0.972)PK | T(-33.19)S(-3 | 0 | 0 | 0 |
| TSPKPT(0.079)KPAS(0.921)PK | T(-51.25)S(-4( | 0 | 0 | 0 |
| VDRS(0.006)DNAAES(0.994)FDDAVEERVI | VDRS(-22.51) | 1 | 0 | 0 |
| VDRS(0.003)DNAAES(0.997)FDDAVEERVI | VDRS(-24.86) | 1 | 0 | 0 |
| VDRS(0.007)DNAAES(0.993)FDDAVEERVI | VDRS(-21.63) | 1 | 0 | 0 |
| VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA | VNS(-28.14)LI | 0 | 0 | 0 |
| VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA | VNS(-29.34)LI | 0 | 0 | 0 |
| VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA | VNS(-31.63)LI | 0 | 0 | 0 |
| VT(0.996)ILWMGGS(0.003) | VTILWM(47.5 | VT(24.72)ILW | 0 | 0 | 0 |
| VT(0.996)ILWMGGS(0.002) | VTILWM(42.3 | VT(27.11)ILW | 0 | 0 | 0 |
| VT(0.999)ILWMGGS(0.001) | VTILWM(42.0 | VT(32.61)ILW | 0 | 0 | 0 |

| Oxidation (M) | Phospho (STY) | Missed cleavages | Proteins | Leading Proteins | Leading Razor Protein | Gene Names |
|---|---|---|---|---|---|---|
| 0 | 2 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 0 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 1 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| 0 | 2 | 1 | M9NG39;P41 | M9NG39 | M9NG39 | Pep |
| | | | | | | Obp22a |
| 1 | 2 | 0 | Q4V3Q5;Q8M | Q4V3Q5 | Q4V3Q5 | CG31941 |
| 1 | 2 | 0 | Q4V3Q5;Q8M | Q4V3Q5 | Q4V3Q5 | Obp22a |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | Q9VUY9 | Q9VUY9 | Q9VUY9 | Pgm |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 2 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 2 | 0 | A0A0B4KHJ5; | A0A0B4KHJ5 | A0A0B4KHJ5 | CG6904-RA;G |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 1 | A0A0B4LGC0, | A0A0B4LGC0 | A0A0B4LGC0 | TppII |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 1 | A0A0B4LGC0 | A0A0B4LGC0 | A0A0B4LGC0 | TppII |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | A0A0B4LFL2;A | A0A0B4LFL2 | A0A0B4LFL2 | eIF3-S8 |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | P45594 | P45594 | P45594 | tsr |
| 0 | 1 | 0 | Q9V5R2;A1Z8 | Q9V5R2 | Q9V5R2 | Pex6 |
| 0 | 1 | 0 | Q9V5R2;A1Z8 | Q9V5R2 | Q9V5R2 | Pex6 |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | B5RJ65;Q053 | B5RJ65 | B5RJ65 | Ssrp-RA;Ssrp |
| 0 | 1 | 0 | Q9VAN0 | Q9VAN0 | Q9VAN0 | CG11899 |
| 0 | 1 | 0 | Q9VAN0 | Q9VAN0 | Q9VAN0 | CG11899 |
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;Aats-glupro-RB |

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|---|---|---|---|---|---|---|
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;A |
| 1 | 1 | 1 | P28668;H8F4 | P28668 | P28668 | Aats-glupro;A |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | |
| 0 | 1 | 0 | Q9VNH5 | Q9VNH5 | Q9VNH5 | |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos |
| 1 | 1 | 0 | Q9VUB8 | Q9VUB8 | Q9VUB8 | endos |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;RpI |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;RpI |
| 1 | 1 | 1 | B7FNN6;P053 | B7FNN6 | B7FNN6 | RpLP2-RB;RpI |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 |
| 0 | 1 | 2 | P05205 | P05205 | P05205 | Su(var)205 |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 |
| 1 | 2 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 |
| 1 | 1 | 2 | M9PBK5;P08! | M9PBK5 | M9PBK5 | RpLP1 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 1 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 1 | 1 | 1 | Q6IIC4 | Q6IIC4 | Q6IIC4 | HDC19000 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 0 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 0 | B7Z0H3 | B7Z0H3 | B7Z0H3 | RhoGEF3 |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 1 | X2JDR1;Q8IR | X2JDR1 | X2JDR1 | CG9413-RB |
| 1 | 1 | 0 | B7YZZ9;P278 | B7YZZ9 | B7YZZ9 | Rrp1 |
| 1 | 1 | 0 | B7YZZ9;P278 | B7YZZ9 | B7YZZ9 | Rrp1 |
| 1 | 1 | 0 | B7YZZ9;P278 | B7YZZ9 | B7YZZ9 | Rrp1 |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 1 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 2 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 2 | Q9VYV4 | Q9VYV4 | Q9VYV4 | Amun |
| 0 | 1 | 2 | Q8IRG6;Q8IR | Q8IRG6 | Q8IRG6 | dre4 |
| 0 | 1 | 2 | Q8IRG6;Q8IR | Q8IRG6 | Q8IRG6 | dre4 |
| 0 | 1 | 2 | Q8IRG6;Q8IR | Q8IRG6 | Q8IRG6 | dre4 |
| 0 | 1 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 |
| 0 | 1 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 |
| 0 | 2 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 |
| 0 | 2 | 0 | E2QCZ8;Q0KI | E2QCZ8 | E2QCZ8 | CG43427 |
| 1 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm |
| 1 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm |
| 0 | 1 | 0 | Q9VIV2;B1NL | Q9VIV2 | Q9VIV2 | swm |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |
| 0 | 1 | 0 | A1Z8W9;A0A | A1Z8W9 | A1Z8W9 | garz |

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|---|---|---|---|---|---|---|
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |
| 0 | 1 | 0 | X2JD55;Q29C | X2JD55 | X2JD55 | Yp1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |
| 0 | 1 | 0 | Q8MYL1 | Q8MYL1 | Q8MYL1 | Fancd2 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |
| 0 | 1 | 0 | Q9VV74 | Q9VV74 | Q9VV74 | Smn |

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|---|---|---|---|---|---|---|
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |
| 0 | 1 | 1 | Q9VZW4;A8V | Q9VZW4 | Q9VZW4 | CG32487 |

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|---|---|---|---|---|---|---|
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |
| 0 | 2 | 0 | A0A0B4KFB8; | A0A0B4KFB8 | A0A0B4KFB8 | CG15187;CG3 |

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|---|---|---|---|---|---|---|
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |
| 0 | 1 | 2 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |
| 0 | 1 | 1 | Q86BM5;Q9V | Q86BM5;Q9V | Q86BM5 | Akap200 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q9I7K6 | Q9I7K6 | Q9I7K6 | CG8223 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 1 | 0 | Q4AB54;P022 | Q4AB54 | Q4AB54 | His1:CG33861 |
| 0 | 1 | 0 | Q4AB54;P022 | Q4AB54 | Q4AB54 | His1:CG33861 |
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 2 | 0 | Q9XZL7;A0AC | Q9XZL7 | Q9XZL7 | tacc |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 |
| 0 | 1 | 0 | Q9V6U8 | Q9V6U8 | Q9V6U8 | Uba3 |
| 0 | 1 | 2 | Q9W335 | Q9W335 | Q9W335 | l(1)G0320 |
| 0 | 1 | 2 | Q9W335 | Q9W335 | Q9W335 | l(1)G0320 |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 |
| 0 | 1 | 0 | C0MJE4;Q24 | C0MJE4 | C0MJE4 | CG4236;Caf1 |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote |
| 0 | 1 | 0 | P20240 | P20240 | P20240 | Ote |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon |
| 1 | 1 | 1 | Q95SA9 | Q95SA9 | Q95SA9 | spoon |

| Protein Names | Type | Labeling State | Raw file | Fraction | Experiment | MS/MS m/z |
|---|---|---|---|---|---|---|
| Zinc finger pr | MULTI-MSMS | | PT5722-2 | 2 | B1 | 761.34 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 761.67 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 735.02 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 734.69 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 777.72 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 777.38 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 804.37 |
| Zinc finger pr | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 804.38 |
| | | | | | | |
| Odorant bind | MSMS | 1 | PT5722-3 | 3 | B1 | 753.86 |
| | MSMS | 1 | PT5722-19 | 19 | B2 | 753.85 |
| | | | | | | |
| Phosphoglucc | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 782.38 |
| Phosphoglucc | MULTI-MSMS | | PT5722-8 | 8 | B1 SCX | 782.38 |
| Phosphoglucc | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 782.05 |
| Phosphoglucc | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 782.38 |
| Phosphoglucc | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 782.38 |
| Phosphoglucc | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 1173.07 |
| Phosphoglucc | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 782.05 |
| Phosphoglucc | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 782.05 |
| Phosphoglucc | MULTI-MATCH | | PT5722-6 | 6 | B1 SCX | |
| Phosphoglucc | MULTI-MATCH | | PT5722-21 | 21 | B2 SCX | |
| Phosphoglucc | MULTI-MATCH | | PT5722-22 | 22 | B2 SCX | |
| Phosphoglucc | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 782.71 |
| | | | | | | |
| Glycogen [sta | MULTI-MSMS | | PT5722-2 | 2 | B1 | 1106.52 |
| Glycogen [sta | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 1106.02 |
| Glycogen [sta | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 1106.03 |
| Glycogen [sta | MULTI-MSMS | | PT5722-47 | 47 | H/H | 1106.52 |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1106.52 |
| Glycogen [sta | MULTI-MATCH | | PT5722-56 | 56 | H/H TIO2 | |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1146.5 |
| Glycogen [sta | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 764.67 |
| | | | | | | |
| Tripeptidyl-pe | ISO-MSMS | 0 | PT5722-6 | 6 | B1 SCX | 943.2 |
| Tripeptidyl-pe | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 943.2 |
| Tripeptidyl-pe | ISO-MSMS | 0 | PT5722-21 | 21 | B2 SCX | 943.2 |
| Tripeptidyl-pe | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 943.2 |

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|---|---|---|---|---|---|
| Tripeptidyl-pe | MULTI-MSMS | | PT5722-51 | 51 H/H SCX | 942.95 |
| | | | | | |
| Eukaryotic tra | MULTI-MSMS | | PT5722-2 | 2 B1 | 841.84 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-6 | 6 B1 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-7 | 7 B1 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-11 | 11 B1 TIO2 | 841.34 |
| Eukaryotic tra | ISO-MSMS | 0 | PT5722-22 | 22 B2 SCX | 841.34 |
| Eukaryotic tra | ISO-MSMS | 0 | PT5722-27 | 27 B2 TIO2 | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-36 | 36 B3 SCX | 841.33 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-37 | 37 B3 SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-41 | 41 B3 TIO2 | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-51 | 51 H/H SCX | 841.34 |
| Eukaryotic tra | MULTI-MSMS | | PT5722-52 | 52 H/H SCX | 841.83 |
| Eukaryotic tra | MULTI-MATCH | | PT5722-42 | 42 B3 TIO2 | |
| | | | | | |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-5 | 5 B1 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-15 | 15 B1 TIO2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-16 | 16 B2 | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-20 | 20 B2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-30 | 30 B2 TIO2 | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-32 | 32 B3 | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-34 | 34 B3 | 622.76 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-49 | 49 H/H | 622.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-50 | 50 H/H | 626.77 |
| Cofilin/actin-( | MULTI-MSMS | | PT5722-60 | 60 H/H TIO2 | 622.76 |
| Cofilin/actin-( | MULTI-MATCH | | PT5722-33 | 33 B3 | |
| | | | | | |
| | MULTI-MSMS | | PT5722-8 | 8 B1 SCX | 619.25 |
| | MULTI-MSMS | | PT5722-23 | 23 B2 SCX | 619.25 |
| | | | | | |
| FACT comple: | ISO-MSMS | 0 | PT5722-6 | 6 B1 SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-7 | 7 B1 SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-22 | 22 B2 SCX | 821.69 |
| FACT comple: | MULTI-MSMS | | PT5722-36 | 36 B3 SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-51 | 51 H/H SCX | 822.02 |
| FACT comple: | MULTI-MSMS | | PT5722-52 | 52 H/H SCX | 822.02 |
| | | | | | |
| Probable pho | MULTI-MSMS | | PT5722-7 | 7 B1 SCX | 388.19 |
| Probable pho | MULTI-SECPEP | | PT5722-37 | 37 B3 SCX | 388.46 |
| | | | | | |
| | | | | | |
| Bifunctional g | ISO-MSMS | 0 | PT5722-21 | 21 B2 SCX | 909.75 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Bifunctional g | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 909.75 |
| Bifunctional g | MULTI-MSMS | | PT5722-51 | 51 | H/H SCX | 909.75 |
| | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 1052.44 |
| | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 1052.78 |
| | ISO-MSMS | 0 | PT5722-53 | 53 | H/H SCX | 1052.78 |
| | ISO-MSMS | 1 | PT5722-10 | 10 | B1 SCX | 707.27 |
| | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 707.27 |
| | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 702.76 |
| 60S acidic rib | MULTI-MSMS | | PT5722-25 | 25 | B2 SCX | 1037.38 |
| 60S acidic rib | ISO-MSMS | 0 | PT5722-45 | 45 | B3 TIO2 | 1037.38 |
| 60S acidic rib | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 1037.38 |
| Heterochrom | ISO-MSMS | 0 | PT5722-9 | 9 | B1 SCX | 727.32 |
| Heterochrom | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 969.42 |
| Heterochrom | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 727.32 |
| Heterochrom | ISO-MSMS | 0 | PT5722-54 | 54 | H/H SCX | 727.32 |
| 60S acidic rib | MSMS | 0 | PT5722-6 | 6 | B1 SCX | 1184.42 |
| 60S acidic rib | MSMS | 0 | PT5722-36 | 36 | B3 SCX | 789.95 |
| 60S acidic rib | MSMS | 0 | PT5722-40 | 40 | B3 SCX | 789.95 |
| 60S acidic rib | MULTI-MSMS | | PT5722-55 | 55 | H/H SCX | 763.63 |
| Protein NASP | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 632.94 |
| Protein NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 632.61 |
| Protein NASP | MULTI-MSMS | | PT5722-32 | 32 | B3 | 632.61 |
| Protein NASP | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 632.94 |
| Protein NASP | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 632.61 |
| Protein NASP | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 632.61 |
| | ISO-MSMS | 1 | PT5722-23 | 23 | B2 SCX | 818.4 |
| | ISO-MSMS | 1 | PT5722-24 | 24 | B2 SCX | 818.4 |
| | ISO-MSMS | 1 | PT5722-38 | 38 | B3 SCX | 817.9 |
| | ISO-MSMS | 1 | PT5722-49 | 49 | H/H | 817.9 |
| | MULTI-MSMS | | PT5722-10 | 10 | B1 SCX | 909.43 |
| | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 609.63 |
| | MULTI-MATCH | | PT5722-23 | 23 | B2 SCX | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 597.63 |

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|---|---|---|---|---|---|---|
| | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 896.44 |
| | MULTI-MATCH | | PT5722-23 | 23 | B2 SCX | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| sobremesa | ISO-MSMS | 1 | PT5722-8 | 8 | B1 SCX | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-9 | 9 | B1 SCX | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-10 | 10 | B1 SCX | 911.44 |
| sobremesa | ISO-MSMS | 1 | PT5722-26 | 26 | B2 TIO2 | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-38 | 38 | B3 SCX | 911.43 |
| sobremesa | ISO-MSMS | 1 | PT5722-40 | 40 | B3 SCX | 911.44 |
| Recombinatic | ISO-MSMS | 0 | PT5722-12 | 12 | B1 TIO2 | 914.74 |
| Recombinatic | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 914.41 |
| Recombinatic | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 914.74 |
| Amun | MULTI-MSMS | | PT5722-2 | 2 | B1 | 555.27 |
| | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 832.41 |
| | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 555.27 |
| | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 832.4 |
| | MULTI-MATCH | | PT5722-36 | 36 | B3 SCX | |
| | MULTI-MSMS | | PT5722-2 | 2 | B1 | 597.97 |
| | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 597.97 |
| FACT comple: | MULTI-MSMS | | PT5722-21 | 21 | B2 SCX | 754.67 |
| FACT comple: | MULTI-MSMS | | PT5722-22 | 22 | B2 SCX | 754.33 |
| FACT comple: | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 754.33 |
| smallish, sma | MULTI-MSMS | | PT5722-24 | 24 | B2 SCX | 558.59 |
| smallish, sma | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 558.58 |
| smallish, sma | MULTI-SECPEP | | PT5722-16 | 16 | B2 | 958.48 |
| smallish, sma | MULTI-SECPEP | | PT5722-33 | 33 | B3 | 958.48 |
| swm | MULTI-MSMS | | PT5722-20 | 20 | B2 | 615.25 |
| | MULTI-MSMS | | PT5722-40 | 40 | B3 SCX | 615.25 |
| | MULTI-MSMS | | PT5722-50 | 50 | H/H | 602.75 |
| garz | ISO-MSMS | 0 | PT5722-6 | 6 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-8 | 8 | B1 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-19 | 19 | B2 | 678.86 |
| | ISO-MSMS | 0 | PT5722-20 | 20 | B2 | 678.86 |
| | ISO-MSMS | 0 | PT5722-21 | 21 | B2 SCX | 678.86 |

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|---|---|---|---|---|---|---|
| | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-24 | 24 | B2 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-31 | 31 | B3 | 678.86 |
| | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 678.86 |
| | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-46 | 46 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-47 | 47 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-50 | 50 | H/H | 678.86 |
| | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 678.86 |
| | ISO-MSMS | 0 | PT5722-54 | 54 | H/H SCX | 678.86 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-8 | 8 | B1 SCX | 717.63 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 717.3 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-33 | 33 | B3 | 717.63 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 717.63 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-40 | 40 | B3 SCX | 717.63 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-48 | 48 | H/H | 720.63 |
| Vitellogenin-1 | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 717.29 |
| Vitellogenin-1 | ISO-MSMS | 0 | PT5722-55 | 55 | H/H SCX | 717.63 |
| Fancd2 | MULTI-MSMS | | PT5722-4 | 4 | B1 | 990.98 |
| | MULTI-MSMS | | PT5722-18 | 18 | B2 | 990.98 |
| | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 990.98 |
| | MULTI-MATCH | | PT5722-24 | 24 | B2 SCX | |
| | MULTI-MATCH | | PT5722-25 | 25 | B2 SCX | |
| Survival motc | ISO-MSMS | 0 | PT5722-24 | 24 | B2 SCX | 1072.48 |
| Survival motc | ISO-MSMS | 0 | PT5722-39 | 39 | B3 SCX | 1072.47 |
| Survival motc | ISO-MSMS | 0 | PT5722-40 | 40 | B3 SCX | 1072.47 |
| CG32487 | ISO-MSMS | 0 | PT5722-2 | 2 | B1 | 753.05 |
| | ISO-MSMS | 0 | PT5722-22 | 22 | B2 SCX | 752.72 |
| | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 753.05 |
| 31367-RA | MULTI-MSMS | | PT5722-23 | 23 | B2 SCX | 670.97 |
| 31367-RA | MULTI-MATCH | | PT5722-21 | 21 | B2 SCX | |
| 31367-RA | MULTI-MATCH | | PT5722-22 | 22 | B2 SCX | |
| Protein NASP | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 727.67 |
| Protein NASP | MULTI-MSMS | | PT5722-7 | 7 | B1 SCX | 546.01 |
| Protein NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 727.68 |

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|---|---|---|---|---|---|---|---|---|
| Protein | NASP | ISO-MSMS | 0 | PT5722-18 | 18 | B2 | 545.76 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 546.01 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 545.76 | |
| Protein | NASP | MULTI-MSMS | | PT5722-36 | 36 | B3 SCX | 728.01 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-36 | 36 | B3 SCX | 546.01 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-37 | 37 | B3 SCX | 727.68 | |

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|---|---|---|---|---|---|---|---|---|
| Akap200 | | ISO-MSMS | 0 | PT5722-9 | 9 | B1 SCX | | 738 |
| Akap200 | | MULTI-MSMS | | PT5722-37 | 37 | B3 SCX | 737.66 | |
| Akap200 | | MULTI-MSMS | | PT5722-39 | 39 | B3 SCX | 737.67 | |
| Akap200 | | ISO-MSMS | 0 | PT5722-47 | 47 | H/H | 737.66 | |
| Akap200 | | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 743.68 | |

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|---|---|---|---|---|---|---|---|---|
| Protein | NASP | MULTI-MSMS | | PT5722-3 | 3 | B1 | 1029.47 | |
| Protein | NASP | MULTI-MSMS | | PT5722-12 | 12 | B1 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-13 | 13 | B1 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-14 | 14 | B1 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-18 | 18 | B2 | 1029.47 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-23 | 23 | B2 SCX | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-27 | 27 | B2 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-28 | 28 | B2 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-29 | 29 | B2 TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-32 | 32 | B3 | 1029.47 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-32 | 32 | B3 | 686.65 | |
| Protein | NASP | MULTI-MSMS | | PT5722-33 | 33 | B3 | 1028.97 | |
| Protein | NASP | MULTI-MSMS | | PT5722-33 | 33 | B3 | 686.32 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 1028.98 | |
| Protein | NASP | MULTI-MSMS | | PT5722-42 | 42 | B3 TIO2 | 1033.48 | |
| Protein | NASP | MULTI-MSMS | | PT5722-42 | 42 | B3 TIO2 | 686.65 | |
| Protein | NASP | MULTI-MSMS | | PT5722-43 | 43 | B3 TIO2 | 1029.47 | |
| Protein | NASP | MULTI-MSMS | | PT5722-44 | 44 | B3 TIO2 | 1028.96 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-44 | 44 | B3 TIO2 | 686.65 | |
| Protein | NASP | ISO-MSMS | 0 | PT5722-45 | 45 | B3 TIO2 | 1028.98 | |
| Protein | NASP | MULTI-MSMS | | PT5722-47 | 47 | H/H | 1029.47 | |
| Protein | NASP | MULTI-MSMS | | PT5722-48 | 48 | H/H | 1028.96 | |
| Protein | NASP | MULTI-MSMS | | PT5722-52 | 52 | H/H SCX | 1028.96 | |
| Protein | NASP | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 1029.47 | |
| Protein | NASP | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 1028.97 | |
| Protein | NASP | MSMS | 0 | PT5722-58 | 58 | H/H TIO2 | 686.32 | |
| Protein | NASP | MULTI-MSMS | | PT5722-59 | 59 | H/H TIO2 | 1028.97 | |
| Protein | NASP | MULTI-MATCH | | PT5722-2 | 2 | B1 | | |

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|---|---|---|---|---|---|---|---|---|
| Histone H1 | | ISO-MSMS | 0 | PT5722-4 | 4 | B1 | 693.66 | |

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|---|---|---|---|---|---|---|
| Histone H1 | ISO-MSMS | 0 | PT5722-19 | 19 | B2 | 1039.49 |
| Histone H1 | MULTI-MSMS | | PT5722-49 | 49 | H/H | 693.33 |
| tacc | ISO-MSMS | 0 | PT5722-7 | 7 | B1 SCX | 826.91 |
| | MULTI-MSMS | | PT5722-41 | 41 | B3 TIO2 | 826.91 |
| | ISO-MSMS | 0 | PT5722-51 | 51 | H/H SCX | 826.9 |
| | MULTI-MSMS | | PT5722-54 | 54 | H/H SCX | 826.9 |
| | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 826.4 |
| | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 866.39 |
| Nedd8-activa | MULTI-MSMS | | PT5722-11 | 11 | B1 TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-28 | 28 | B2 TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-57 | 57 | H/H TIO2 | 799.9 |
| Nedd8-activa | MULTI-MSMS | | PT5722-58 | 58 | H/H TIO2 | 799.9 |
| | MULTI-MSMS | | PT5722-19 | 19 | B2 | 440.23 |
| | MULTI-MSMS | | PT5722-34 | 34 | B3 | 440.56 |
| Probable hist | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 1008.44 |
| Probable hist | MULTI-MSMS | | PT5722-38 | 38 | B3 SCX | 1008.44 |
| Probable hist | MULTI-MSMS | | PT5722-53 | 53 | H/H SCX | 1008.77 |
| Otefin | ISO-MSMS | 0 | PT5722-3 | 3 | B1 | 954.95 |
| Otefin | ISO-MSMS | 0 | PT5722-33 | 33 | B3 | 954.96 |
| Otefin | ISO-MSMS | 0 | PT5722-38 | 38 | B3 SCX | 954.96 |
| spoon | MULTI-MSMS | | PT5722-4 | 4 | B1 | 672.02 |
| | MULTI-MSMS | | PT5722-18 | 18 | B2 | 672.02 |
| | MULTI-MSMS | | PT5722-32 | 32 | B3 | 671.69 |

| Charge | m/z | Mass | Resolution | Uncalibrated - Calibrated m/z [ppm] | Uncalibrated - Calibrated m/z [Da] | Mass Error [ppm] |
|---|---|---|---|---|---|---|
| 3 | 761,341,567 | 228,100,287 | 48700.75 | -0.6341 | -0.00048276 | -0.040968 |
| 3 | 761,341,567 | 228,100,287 | NaN | NaN | NaN | 0.14489 |
| 3 | 734,686,124 | 220,103,654 | NaN | NaN | NaN | 0.91062 |
| 3 | 734,686,124 | 220,103,654 | NaN | NaN | NaN | 0.23012 |
| 3 | 777,384,445 | 23,291,315 | NaN | NaN | NaN | 0.8582 |
| 3 | 777,384,445 | 23,291,315 | NaN | NaN | NaN | 0.78236 |
| 3 | 804,039,888 | 240,909,784 | NaN | NaN | NaN | 0.47731 |
| 3 | 804,039,888 | 240,909,784 | NaN | NaN | NaN | 0.28295 |
| 2 | 749,842,461 | 149,767,037 | NaN | NaN | NaN | NaN |
| 2 | 749,842,461 | 149,767,037 | NaN | NaN | NaN | NaN |
| 3 | 782,049,285 | 234,312,603 | 49084.29 | -0.31035 | -0.00024271 | -0.22733 |
| 3 | 782,049,285 | 234,312,603 | 47136.54 | -0.6614 | -0.00051725 | -0.84304 |
| 3 | 782,049,285 | 234,312,603 | 48041.27 | -0.65958 | -0.00051582 | -0.34588 |
| 3 | 782,049,285 | 234,312,603 | NaN | NaN | NaN | 0.32247 |
| 3 | 782,049,285 | 234,312,603 | 47180.82 | -0.58054 | -0.00045401 | -0.46054 |
| 2 | 117,257,029 | 234,312,603 | 38721.94 | -0.93501 | -0.0010964 | -0.19664 |
| 3 | 782,049,285 | 234,312,603 | NaN | NaN | NaN | -0.60707 |
| 3 | 782,049,285 | 234,312,603 | 47256.8 | -0.42933 | -0.00033576 | -0.70423 |
| 3 | 782,049,285 | 234,312,603 | 47104.99 | -0.85091 | -0.00066545 | -0.34612 |
| 3 | 782,049,285 | 234,312,603 | 46783.95 | -0.96112 | -0.00075164 | -0.95532 |
| 3 | 782,049,285 | 234,312,603 | 47026.67 | -0.66347 | -0.00051887 | -0.428 |
| 3 | 78,237,729 | 234,411,004 | NaN | NaN | NaN | 0.13328 |
| 2 | 110,601,649 | 221,001,843 | 40031.52 | -0.93809 | -0.0010375 | 0.17847 |
| 2 | 110,601,649 | 221,001,843 | 39980.95 | -0.7294 | -0.00080672 | 0.064339 |
| 2 | 110,601,649 | 221,001,843 | NaN | NaN | NaN | 0.45069 |
| 2 | 110,601,649 | 221,001,843 | 40122.95 | -0.48689 | -0.00053851 | 0.11751 |
| 2 | 110,601,649 | 221,001,843 | 39421.7 | -0.60565 | -0.00066986 | 0.046545 |
| 2 | 110,601,649 | 221,001,843 | 39367.34 | 0 | 0 | -0.48324 |
| 2 | 114,599,966 | 228,998,476 | 40352.94 | -0.60563 | -0.00069406 | 0.03998 |
| 3 | 764,335,531 | 228,998,476 | 48247.85 | -0.60554 | -0.00046284 | -0.14232 |
| 4 | 942,699,453 | 376,676,871 | NaN | NaN | NaN | 0.7398 |
| 4 | 942,699,453 | 376,676,871 | NaN | NaN | NaN | 0.44133 |
| 4 | 942,699,453 | 376,676,871 | NaN | NaN | NaN | 0.57015 |
| 4 | 942,699,453 | 376,676,871 | NaN | NaN | NaN | 0.62828 |

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|---|---|---|---|---|---|---|
| 4 | 942,699,453 | 376,676,871 | 43554.6 | -0.24396 | -0.00022998 | -11,793 |
| 2 | 84,133,509 | 168,065,563 | 45027.15 | -0.89245 | -0.00075085 | 0.41865 |
| 2 | 84,133,509 | 168,065,563 | 44767.33 | -0.58062 | -0.0004885 | -0.38377 |
| 2 | 84,133,509 | 168,065,563 | 44982.43 | -0.63029 | -0.00053029 | 0.24525 |
| 2 | 84,133,509 | 168,065,563 | 45711.25 | 0 | 0 | -11,744 |
| 2 | 84,133,509 | 168,065,563 | NaN | NaN | NaN | 0.69875 |
| 2 | 84,133,509 | 168,065,563 | NaN | NaN | NaN | -0.11447 |
| 2 | 84,133,509 | 168,065,563 | 43560.81 | -0.47621 | -0.00040065 | -0.33956 |
| 2 | 84,133,509 | 168,065,563 | 45250.93 | -0.87036 | -0.00073227 | -0.046635 |
| 2 | 84,133,509 | 168,065,563 | 45688.7 | -0.94427 | -0.00079445 | -0.28334 |
| 2 | 84,133,509 | 168,065,563 | 46313.07 | -0.57953 | -0.00048758 | -0.35958 |
| 2 | 84,133,509 | 168,065,563 | 45818.69 | -0.70187 | -0.0005905 | -0.055655 |
| 2 | 84,133,509 | 168,065,563 | 46058.67 | -0.88319 | -0.00074306 | 0.088149 |
| 2 | 622,765,061 | 124,351,557 | 49666.66 | -11,675 | -0.00072709 | 0.72062 |
| 2 | 622,765,061 | 124,351,557 | 53750.39 | 0 | 0 | -0.36105 |
| 2 | 622,765,061 | 124,351,557 | 53765.87 | -0.68807 | -0.00042851 | -0.096821 |
| 2 | 622,765,061 | 124,351,557 | 49223.58 | -0.70701 | -0.0004403 | 0.21521 |
| 2 | 622,765,061 | 124,351,557 | 53622.12 | 0 | 0 | -0.33432 |
| 2 | 622,765,061 | 124,351,557 | 52022.43 | -0.23251 | -0.0001448 | -0.28415 |
| 2 | 622,765,061 | 124,351,557 | 53283.96 | -0.8521 | -0.00053066 | -0.026131 |
| 2 | 622,765,061 | 124,351,557 | 54265.55 | -0.51174 | -0.0003187 | 0.47838 |
| 2 | 622,765,061 | 124,351,557 | 49801.67 | -0.35894 | -0.00022353 | 0.1143 |
| 2 | 622,765,061 | 124,351,557 | 53179.15 | -0.50061 | -0.00031176 | 0.29178 |
| 2 | 622,765,061 | 124,351,557 | 54084.26 | -0.31982 | -0.00019917 | -0.43446 |
| 2 | 619,254,852 | 123,649,515 | 53106.32 | -0.21324 | -0.00013205 | 13,032 |
| 2 | 619,254,852 | 123,649,515 | 51842.47 | -0.24336 | -0.0001507 | 15,959 |
| 3 | 821,683,108 | 246,202,749 | NaN | NaN | NaN | 0.72795 |
| 3 | 821,683,108 | 246,202,749 | 46390.55 | -0.52842 | -0.00043419 | 0.18359 |
| 3 | 821,683,108 | 246,202,749 | 46712.96 | -0.49176 | -0.00040407 | -0.048026 |
| 3 | 821,683,108 | 246,202,749 | 46631.54 | -0.5666 | -0.00046556 | 0.12942 |
| 3 | 821,683,108 | 246,202,749 | 46837.07 | -0.46708 | -0.00038379 | -0.087081 |
| 3 | 821,683,108 | 246,202,749 | 46733.58 | -0.54819 | -0.00045044 | -0.36846 |
| 4 | 385,940,632 | 153,973,342 | 66420.11 | 0.018018 | 6.95E-02 | -13,849 |
| 4 | 385,940,632 | 153,973,342 | 66350.92 | -0.27129 | -0.0001047 | -13,766 |
| 3 | 9,094,124 | 272,521,537 | NaN | NaN | NaN | 0.53441 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 3 | 9,094,124 | 272,521,537 | NaN | NaN | NaN | 0.7078 |
| | 3 | 9,094,124 | 272,521,537 | 44209.95 | -0.57909 | -0.00052663 | 0.11881 |
| | 3 | 105,211,134 | 315,331,218 | NaN | NaN | NaN | 0.088838 |
| | 3 | 105,211,134 | 315,331,218 | NaN | NaN | NaN | -0.079777 |
| | 3 | 105,211,134 | 315,331,218 | NaN | NaN | NaN | 0.38664 |
| | 2 | 702,762,518 | 140,351,048 | NaN | NaN | NaN | -14,181 |
| | 2 | 702,762,518 | 140,351,048 | 49509.86 | -0.77163 | -0.00054227 | -0.70452 |
| | 2 | 702,762,518 | 140,351,048 | 50982.97 | -0.46099 | -0.00032397 | 0.016504 |
| | 2 | 103,737,957 | 207,274,458 | 41426.96 | -0.80348 | -0.00083351 | -0.3003 |
| | 2 | 103,737,957 | 207,274,458 | NaN | NaN | NaN | 0.01813 |
| | 2 | 103,737,957 | 207,274,458 | 41640.52 | -0.73718 | -0.00076473 | -0.066447 |
| | 4 | 727,068,215 | 290,424,375 | NaN | NaN | NaN | 10,117 |
| | 3 | 969,088,528 | 290,424,375 | 42884.98 | -11,746 | -0.0011383 | -0.24134 |
| | 4 | 727,068,215 | 290,424,375 | 49911.34 | -0.99858 | -0.00072604 | -0.1016 |
| | 4 | 727,068,215 | 290,424,375 | NaN | NaN | NaN | 0.51106 |
| | 2 | 118,441,603 | 23,668,175 | NaN | NaN | NaN | NaN |
| | 3 | 789,946,443 | 23,668,175 | NaN | NaN | NaN | NaN |
| | 3 | 789,946,443 | 23,668,175 | NaN | NaN | NaN | NaN |
| | 3 | 763,290,999 | 228,685,117 | 47898.98 | -0.71276 | -0.00054404 | -0.16419 |
| | 3 | 632,607,934 | 189,480,197 | NaN | NaN | NaN | 10,578 |
| | 3 | 632,607,934 | 189,480,197 | 52561.09 | -0.94823 | -0.00059985 | -0.19406 |
| | 3 | 632,607,934 | 189,480,197 | 54769.45 | -0.55402 | -0.00035048 | 0.0018982 |
| | 3 | 632,607,934 | 189,480,197 | NaN | NaN | NaN | 0.58237 |
| | 3 | 632,607,934 | 189,480,197 | NaN | NaN | NaN | 0.64711 |
| | 3 | 632,607,934 | 189,480,197 | 52791.61 | -0.51669 | -0.00032686 | -0.51163 |
| | 2 | 809,886,573 | 161,775,859 | NaN | NaN | NaN | -13,628 |
| | 2 | 809,886,573 | 161,775,859 | NaN | NaN | NaN | -0.79476 |
| | 2 | 809,886,573 | 161,775,859 | NaN | NaN | NaN | -11,434 |
| | 2 | 809,886,573 | 161,775,859 | NaN | NaN | NaN | -15,373 |
| | 2 | 909,435,761 | 181,685,697 | 43696.7 | -18,642 | -0.0016954 | 0.0030465 |
| | 3 | 606,626,266 | 181,685,697 | 52622.78 | -0.53676 | -0.00032561 | -11,913 |
| | 3 | 606,626,266 | 181,685,697 | 53944.11 | -0.10199 | -6.19E-01 | -12,749 |
| | 3 | 606,626,266 | 181,685,697 | 53182.92 | -0.37484 | -0.00022739 | -10,728 |
| | 3 | 597,626,378 | 17,898,573 | 52584.19 | -0.2817 | -0.00016835 | -0.85859 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2 | 895,935,928 | 17,898,573 | 42945.04 | -0.27722 | -0.00024837 | -17,824 |
| 2 | 895,935,928 | 17,898,573 | 43884.54 | -11,219 | -0.0010051 | -0.50313 |
| 3 | 597,626,378 | 17,898,573 | 51025.32 | -0.64456 | -0.00038521 | -0.27575 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 0.48176 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 12,271 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 17,114 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 0.061222 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 13,955 |
| 2 | 903,419,923 | 180,482,529 | NaN | NaN | NaN | 14,456 |
| 3 | 914,401,501 | 274,018,267 | NaN | NaN | NaN | -0.36446 |
| 3 | 914,401,501 | 274,018,267 | NaN | NaN | NaN | 0.40981 |
| 3 | 914,401,501 | 274,018,267 | 43868.11 | -0.60547 | -0.00055364 | -0.39734 |
| 3 | 555,273,215 | 166,279,782 | 57588.13 | -0.64389 | -0.00035753 | -0.39201 |
| 2 | 832,406,184 | 166,279,782 | 45805.02 | -0.90136 | -0.0007503 | -0.30556 |
| 3 | 555,273,215 | 166,279,782 | 57856 | -0.18944 | -0.00010519 | -0.24905 |
| 2 | 832,406,184 | 166,279,782 | 45675.85 | -0.69867 | -0.00058158 | 0.5334 |
| 2 | 832,406,184 | 166,279,782 | 47421.39 | -0.78716 | -0.00065524 | -0.099439 |
| 3 | 597,971,536 | 179,089,278 | 53542.4 | -0.51142 | -0.00030581 | -11,847 |
| 3 | 597,971,536 | 179,089,278 | 52488.26 | -0.45983 | -0.00027496 | -13,331 |
| 3 | 754,333,416 | 225,997,842 | 48501.36 | -12,935 | -0.00097576 | 0.59531 |
| 3 | 754,333,416 | 225,997,842 | 48648.12 | -0.68361 | -0.00051567 | 0.44713 |
| 3 | 754,333,416 | 225,997,842 | 47620.15 | -0.6986 | -0.00052698 | 0.019261 |
| 3 | 558,251,534 | 167,173,277 | 52879.02 | -0.43009 | -0.0002401 | 0.60775 |
| 3 | 558,579,539 | 167,271,679 | NaN | NaN | NaN | 10,397 |
| 2 | 958,475,759 | 191,493,696 | 42446.84 | -10,427 | -0.00099945 | 14,035 |
| 2 | 958,475,759 | 191,493,696 | 42782.33 | -0.13625 | -0.0001306 | 10,331 |
| 2 | 610,743,263 | 121,947,197 | 52952.65 | -0.76413 | -0.00046669 | -12,932 |
| 2 | 610,743,263 | 121,947,197 | 52520.14 | -0.41241 | -0.00025187 | -14,579 |
| 2 | 602,745,805 | 120,347,706 | 53745.4 | -0.83504 | -0.00050332 | -11,888 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.15588 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.50484 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.68469 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.20306 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.24851 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.2432 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -10,303 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.52289 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.85876 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.46929 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.22617 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.41926 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.37923 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -10,336 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.5864 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.89777 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.80944 |
| 2 | 678,862,361 | 135,571,017 | NaN | NaN | NaN | -0.39322 |
| 3 | 71,729,563 | 214,886,506 | NaN | NaN | NaN | 10,651 |
| 3 | 71,729,563 | 214,886,506 | NaN | NaN | NaN | 0.96299 |
| 3 | 71,729,563 | 214,886,506 | 50576.19 | -0.81753 | -0.00058641 | -0.5649 |
| 3 | 71,729,563 | 214,886,506 | 48931.68 | -11,873 | -0.00085165 | -0.36907 |
| 3 | 71,729,563 | 214,886,506 | NaN | NaN | NaN | 0.82332 |
| 3 | 71,729,563 | 214,886,506 | 48935.83 | -0.89124 | -0.00063928 | -0.42935 |
| 3 | 71,729,563 | 214,886,506 | 48589.26 | -0.93498 | -0.00067066 | -0.48078 |
| 3 | 71,729,563 | 214,886,506 | NaN | NaN | NaN | 0.61346 |
| 2 | 990,473,732 | 197,893,291 | 41371.02 | -0.13943 | -0.0001381 | 1,129 |
| 2 | 990,473,732 | 197,893,291 | 41700.63 | -0.8848 | -0.00087637 | 17,107 |
| 2 | 990,473,732 | 197,893,291 | 41721.6 | -0.71732 | -0.00071049 | 15,135 |
| 2 | 990,473,732 | 197,893,291 | 41596.73 | -0.78942 | -0.0007819 | 10,194 |
| 2 | 990,473,732 | 197,893,291 | 41791.86 | -0.78107 | -0.00077363 | 1,597 |
| 3 | 107,214,017 | 321,339,869 | NaN | NaN | NaN | 10,075 |
| 3 | 107,214,017 | 321,339,869 | NaN | NaN | NaN | 11,244 |
| 3 | 107,214,017 | 321,339,869 | NaN | NaN | NaN | 0.064241 |
| 3 | 752,716,813 | 225,512,861 | NaN | NaN | NaN | 0.39857 |
| 3 | 752,716,813 | 225,512,861 | NaN | NaN | NaN | 0.6837 |
| 3 | 752,716,813 | 225,512,861 | NaN | NaN | NaN | 0.95028 |
| 3 | 670,304,899 | 200,789,287 | 50782.59 | -12,919 | -0.00086598 | -14,228 |
| 3 | 670,304,899 | 200,789,287 | 50413.44 | -0.92069 | -0.00061714 | -23,988 |
| 3 | 670,304,899 | 200,789,287 | 49867.72 | -0.80455 | -0.00053929 | -22,151 |
| 3 | 727,339,959 | 217,899,805 | NaN | NaN | NaN | 0.67973 |
| 4 | 545,756,788 | 217,899,805 | 55200.6 | -0.47673 | -0.00026018 | -11,118 |
| 3 | 727,339,959 | 217,899,805 | 47298.66 | -1,453 | -0.0010568 | -0.28561 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 4 | 545,756,788 | 217,899,805 | NaN | NaN | NaN | | 10,085 |
| 4 | 545,756,788 | 217,899,805 | NaN | NaN | NaN | | 0.51477 |
| 4 | 545,756,788 | 217,899,805 | NaN | NaN | NaN | | 0.43893 |
| 3 | 727,339,959 | 217,899,805 | 49461.57 | -0.8152 | -0.00059293 | | -0.26477 |
| 4 | 545,756,788 | 217,899,805 | NaN | NaN | NaN | | 0.29208 |
| 3 | 727,339,959 | 217,899,805 | NaN | NaN | NaN | | 0.67912 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 3 | 737,665,277 | 2,209,974 | NaN | NaN | NaN | | 0.7087 |
| 3 | 737,665,277 | 2,209,974 | 48021.57 | -0.81164 | -0.00059872 | | -1,022 |
| 3 | 737,665,277 | 2,209,974 | 49666.97 | -0.73257 | -0.00054039 | | -0.59356 |
| 3 | 737,665,277 | 2,209,974 | NaN | NaN | NaN | | 0.063042 |
| 3 | 737,665,277 | 2,209,974 | 48325.57 | -0.67641 | -0.00049896 | | -0.688 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2 | 102,896,974 | 205,592,493 | 40445.55 | -0.72577 | -0.0007468 | | -0.46537 |
| 2 | 102,896,974 | 205,592,493 | 40108.64 | 0 | 0 | | -17,689 |
| 2 | 102,896,974 | 205,592,493 | 40719.98 | 0 | 0 | | -16,878 |
| 2 | 102,896,974 | 205,592,493 | 42294.86 | 0 | 0 | | -15,537 |
| 2 | 102,896,974 | 205,592,493 | 40144.92 | -0.4439 | -0.00045676 | | -10,553 |
| 2 | 102,896,974 | 205,592,493 | NaN | NaN | NaN | | 0.40686 |
| 2 | 102,896,974 | 205,592,493 | 40656.43 | 0 | 0 | | -17,644 |
| 2 | 102,896,974 | 205,592,493 | 40637.25 | 0 | 0 | | -16,164 |
| 2 | 102,896,974 | 205,592,493 | 41381.46 | 0 | 0 | | -11,285 |
| 2 | 102,896,974 | 205,592,493 | 40644.64 | -0.15679 | -0.00016133 | | -12,504 |
| 3 | 686,315,585 | 205,592,493 | NaN | NaN | NaN | | 0.93733 |
| 2 | 102,896,974 | 205,592,493 | 41106.15 | -0.72335 | -0.0007443 | | -0.40616 |
| 3 | 686,315,585 | 205,592,493 | 50304.32 | -0.18577 | -0.0001275 | | -0.72788 |
| 2 | 102,896,974 | 205,592,493 | NaN | NaN | NaN | | 0.12316 |
| 2 | 102,896,974 | 205,592,493 | 40951.85 | -0.88397 | -0.00090958 | | -0.59491 |
| 3 | 686,315,585 | 205,592,493 | 50827.29 | -0.88301 | -0.00060602 | | 0.062175 |
| 2 | 102,896,974 | 205,592,493 | 40977.51 | 0 | 0 | | -14,647 |
| 2 | 102,896,974 | 205,592,493 | 41019.25 | 0 | 0 | | -13,648 |
| 3 | 686,315,585 | 205,592,493 | NaN | NaN | NaN | | 0.036765 |
| 2 | 102,896,974 | 205,592,493 | NaN | NaN | NaN | | -0.070952 |
| 2 | 102,896,974 | 205,592,493 | 41467.31 | -0.1204 | -0.00012389 | | -0.57332 |
| 2 | 102,896,974 | 205,592,493 | 41073.05 | -0.52115 | -0.00053625 | | 0.11019 |
| 2 | 102,896,974 | 205,592,493 | 42349.81 | -0.25346 | -0.0002608 | | -0.58571 |
| 2 | 102,896,974 | 205,592,493 | 41294.95 | -0.6056 | -0.00062315 | | -0.12905 |
| 2 | 102,896,974 | 205,592,493 | 41438.02 | 0 | 0 | | -0.67687 |
| 3 | 686,315,585 | 205,592,493 | NaN | NaN | NaN | | NaN |
| 2 | 102,896,974 | 205,592,493 | 41382.49 | 0 | 0 | | -0.21612 |
| 2 | 102,896,974 | 205,592,493 | 40875.37 | -0.67242 | -0.0006919 | | -0.46279 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 3 | 693,327,825 | 207,696,165 | NaN | NaN | NaN | | 0.95663 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2 | 10,394,881 | 207,696,165 | NaN | NaN | NaN | 0.78001 | |
| 3 | 693,327,825 | 207,696,165 | 51124.58 | -0.24826 | -0.00017213 | -0.90324 | |
| 2 | 826,402,579 | 16,507,906 | NaN | NaN | NaN | 19,666 | |
| 2 | 826,402,579 | 16,507,906 | 44413.07 | -0.71751 | -0.00059296 | -0.17386 | |
| 2 | 826,402,579 | 16,507,906 | NaN | NaN | NaN | 20,438 | |
| 2 | 826,402,579 | 16,507,906 | 44639.39 | -0.90043 | -0.00074412 | 0.59597 | |
| 2 | 826,402,579 | 16,507,906 | 45362.56 | -0.6055 | -0.00050038 | 0.23264 | |
| 2 | 866,385,744 | 173,075,693 | 46475.25 | -0.60516 | -0.0005243 | 0.48461 | |
| 2 | 799,900,538 | 159,778,652 | 45334.03 | 0 | 0 | -14,209 | |
| 2 | 799,900,538 | 159,778,652 | 49691.38 | 0 | 0 | -0.59866 | |
| 2 | 799,900,538 | 159,778,652 | 47238.11 | -0.60566 | -0.00048447 | 0.065684 | |
| 2 | 799,900,538 | 159,778,652 | 46978.66 | 0 | 0 | -0.66459 | |
| 3 | 440,230,399 | 131,766,937 | 62752.88 | -0.20477 | -9.01E-01 | -0.60419 | |
| 3 | 440,230,399 | 131,766,937 | 62672.29 | -0.27832 | -0.00012253 | 0.42741 | |
| 3 | 100,810,317 | 302,128,768 | NaN | NaN | NaN | 0.81854 | |
| 3 | 100,810,317 | 302,128,768 | 41498.1 | -0.1923 | -0.00019385 | -0.69867 | |
| 3 | 100,810,317 | 302,128,768 | 41709.66 | -0.69225 | -0.00069786 | -0.24163 | |
| 4 | 954,455,923 | 381,379,459 | NaN | NaN | NaN | -0.43112 | |
| 4 | 954,455,923 | 381,379,459 | NaN | NaN | NaN | 0.51079 | |
| 4 | 954,455,923 | 381,379,459 | NaN | NaN | NaN | 0.73047 | |
| 3 | 67,168,786 | 201,204,175 | 51096.34 | -0.04967 | -3.34E-01 | 17,197 | |
| 3 | 67,168,786 | 201,204,175 | 50391.08 | 0.0094576 | 6.35E-02 | 19,131 | |
| 3 | 67,168,786 | 201,204,175 | 47925.68 | 0.24981 | 0.0001678 | 13,833 | |

| Mass Error [Da] | Uncalibrated Mass Error [ppm] | Uncalibrated Mass Error [Da] | Max intensity m/z 0 | Max intensity m/z 1 | Retention time | Retention length |
|---|---|---|---|---|---|---|
| -3.12E-02 | -0.67506 | -0.00051395 | ########## | ########## | 73,595 | 0.60837 |
| 0.00011031 | NaN | NaN | NaN | NaN | 78,863 | 0.81698 |
| 0.00066902 | NaN | NaN | NaN | NaN | 67,212 | 0.58141 |
| 0.00016907 | NaN | NaN | NaN | NaN | 71,066 | 10,799 |
| 0.00066715 | NaN | NaN | NaN | NaN | 58,525 | 0.57363 |
| 0.0006082 | NaN | NaN | NaN | NaN | 63,039 | 0.88077 |
| 0.00038378 | NaN | NaN | NaN | NaN | 63,152 | 0.58234 |
| 0.0002275 | NaN | NaN | NaN | NaN | 67,438 | 0.67523 |
| | | | | | | |
| NaN | NaN | NaN | NaN | NaN | 73,177 | 1 |
| NaN | NaN | NaN | NaN | NaN | 73,417 | 1 |
| -0.00017778 | -0.53768 | -0.00042049 | ########## | ########## | 103.41 | 0.57672 |
| -0.0006593 | -15,044 | -0.0011765 | ########## | ########## | 100.42 | 0.85462 |
| -0.0002705 | -10,055 | -0.00078632 | ########## | ########## | 97,275 | 10,631 |
| 0.00025218 | NaN | NaN | NaN | NaN | 102.37 | 19,762 |
| -0.00036016 | -10,411 | -0.00081417 | ########## | ########## | 97,438 | 0.64938 |
| -0.00023058 | -11,317 | -0.0013269 | ########## | ########## | 97,415 | 0.58425 |
| -0.00047476 | NaN | NaN | NaN | NaN | 102.5 | 13,302 |
| -0.00055074 | -11,336 | -0.0008865 | ########## | ########## | 97.99 | 10,517 |
| -0.00027068 | -1,197 | -0.00093614 | ########## | ########## | 105.34 | 0.73146 |
| -0.00074711 | -19,164 | -0.0014987 | ########## | ########## | 100.21 | 0.42425 |
| -0.00033472 | -10,915 | -0.00085358 | ########## | ########## | 98.64 | 0.56222 |
| 0.00010427 | NaN | NaN | NaN | NaN | 98,032 | 0.47295 |
| 0.00019739 | -0.75963 | -0.00084016 | ########## | ########## | 116.29 | 0.62392 |
| 7.12E-02 | -0.66506 | -0.00073556 | ########## | ########## | 119.5 | 0.31782 |
| 0.00049847 | NaN | NaN | NaN | NaN | 126.64 | 0.47802 |
| 0.00012997 | -0.36938 | -0.00040854 | ########## | ########## | 136.54 | 0.56355 |
| 5.15E-01 | -0.55911 | -0.00061838 | ########## | ########## | 116.89 | 0.64877 |
| -0.00053448 | -0.48324 | -0.00053448 | ########## | ########## | 117.13 | 0.53051 |
| 4.58E-01 | -0.56565 | -0.00064824 | ########## | ########## | 126.86 | 0.8235 |
| -0.00010878 | -0.74786 | -0.00057162 | ########## | ########## | 126.92 | 0.62176 |
| 0.00069741 | NaN | NaN | NaN | NaN | 79,829 | 0.67028 |
| 0.00041604 | NaN | NaN | NaN | NaN | 78,767 | 0.8231 |
| 0.00053748 | NaN | NaN | NaN | NaN | 77,134 | 0.60345 |
| 0.00059228 | NaN | NaN | NaN | NaN | 81,341 | 14,287 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| -0.0011118 | -14,233 | -0.0013418 | ########## | ########## | 78.16 | | 10,275 |
| 0.00035223 | -0.47379 | -0.00039862 | ########## | ########## | | 81,717 | 0.60141 |
| -0.00032288 | -0.9644 | -0.00081138 | ########## | ########## | | 85,461 | 0.54626 |
| 0.00020634 | -0.38504 | -0.00032395 | ########## | ########## | | 84,705 | 0.659 |
| -0.00098804 | -11,744 | -0.00098804 | ########## | ########## | | 81,916 | 0.5723 |
| 0.00058788 | NaN | NaN | NaN | NaN | | 83,036 | 0.60281 |
| -9.63E-01 | NaN | NaN | NaN | NaN | | 81,405 | 0.53769 |
| -0.00028568 | -0.81577 | -0.00068633 | ########## | ########## | | 95,193 | 0.4995 |
| -3.92E-01 | -0.917 | -0.0007715 | ########## | ########## | | 94,723 | 0.63361 |
| -0.00023838 | -12,276 | -0.0010328 | ########## | ########## | | 82,131 | 0.55059 |
| -0.00030253 | -0.93911 | -0.00079011 | ########## | ########## | | 84,447 | 0.58243 |
| -4.68E-01 | -0.75752 | -0.00063733 | ########## | ########## | | 83,209 | 0.60301 |
| 7.42E-01 | -0.79504 | -0.00066889 | ########## | ########## | | 81,927 | 0.48901 |
| 0.00044878 | -0.44689 | -0.00027831 | ########## | ########## | | 76,755 | 15,688 |
| -0.00022485 | -0.36105 | -0.00022485 | ########## | ########## | | 76,205 | 0.73231 |
| -6.03E-01 | -0.78489 | -0.0004888 | ########## | ########## | | 76,587 | 0.50031 |
| 0.00013403 | -0.4918 | -0.00030627 | ########## | ########## | | 77,517 | 13,885 |
| -0.00020821 | -0.33432 | -0.00020821 | ########## | ########## | | 77,719 | 0.58629 |
| -0.00017696 | -0.51667 | -0.00032176 | ########## | ########## | | 87,667 | 0.53617 |
| -1.63E-01 | -0.87823 | -0.00054693 | ########## | ########## | | 87,765 | 0.65209 |
| 0.00029792 | -0.033363 | -2.08E-01 | ########## | ########## | | 78,112 | 0.86717 |
| 7.12E-01 | -0.24463 | -0.00015235 | ########## | ########## | | 76,455 | 16,749 |
| 0.00018171 | -0.20884 | -0.00013006 | ########## | ########## | | 78,722 | 0.7103 |
| -0.00027057 | -0.75428 | -0.00046974 | ########## | ########## | | 87,866 | 0.6384 |
| 0.000807 | 10,899 | 0.00067495 | ########## | ########## | | 94,877 | 0.67711 |
| 0.00098824 | 13,525 | 0.00083754 | ########## | ########## | | 94,214 | 0.52608 |
| 0.00059814 | NaN | NaN | NaN | NaN | 103.01 | | 0.75828 |
| 0.00015085 | -0.34483 | -0.00028334 | ########## | ########## | 101.81 | | 0.72246 |
| -3.95E-01 | -0.53978 | -0.00044353 | ########## | ########## | 100.02 | | 0.75243 |
| 0.00010634 | -0.43717 | -0.00035922 | ########## | ########## | 110.97 | | 10,815 |
| -7.16E-01 | -0.55416 | -0.00045534 | ########## | ########## | 102.64 | | 0.68706 |
| -0.00030275 | -0.91665 | -0.0007532 | ########## | ########## | 101.37 | | 0.67909 |
| -0.00053448 | -13,669 | -0.00052752 | ########## | ########## | | 51,006 | 0.59747 |
| -0.0005313 | -16,479 | -0.000636 | ########## | ########## | | 57,204 | 0.60443 |
| 0.000486 | NaN | NaN | NaN | NaN | | 78,509 | 0.36842 |

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|---|---|---|---|---|---|---|---|
| 0.00064369 | NaN | NaN | NaN | NaN | | 87,301 | 0.7648 |
| 0.00010804 | -0.46028 | -0.00041858 | ########## | ########## | | 79,768 | 0.59363 |

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|---|---|---|---|---|---|---|---|
| 9.35E-01 | NaN | NaN | NaN | NaN | | 88,133 | 0.81361 |
| -8.39E-01 | NaN | NaN | NaN | NaN | 88.65 | | 0.6924 |
| 0.00040679 | NaN | NaN | NaN | NaN | 88.85 | | 0.88759 |

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|---|---|---|---|---|---|---|---|
| -0.00099659 | NaN | NaN | NaN | NaN | | 70,489 | 0.52867 |
| -0.00049511 | -14,762 | -0.0010374 | ########## | ########## | | 71,545 | 0.62837 |
| 1.16E-01 | -0.44449 | -0.00031237 | ########## | ########## | | 70,618 | 0.64713 |

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|---|---|---|---|---|---|---|---|
| -0.00031152 | -11,038 | -0.001145 | ########## | ########## | 108.15 | | 0.59637 |
| 1.88E-01 | NaN | NaN | NaN | NaN | 108.99 | | 0.44384 |
| -6.89E-01 | -0.80363 | -0.00083366 | ########## | ########## | 108.84 | | 0.54576 |

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|---|---|---|---|---|---|---|---|
| 0.00073559 | NaN | NaN | NaN | NaN | | 66,421 | 0.63902 |
| -0.00023388 | -1,416 | -0.0013722 | ########## | ########## | | 64,623 | 0.91163 |
| -7.39E-01 | -11,002 | -0.00079991 | ########## | ########## | | 64,653 | 0.91163 |
| 0.00037158 | NaN | NaN | NaN | NaN | | 64,588 | 0.61862 |

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|---|---|---|---|---|---|---|---|
| NaN | NaN | NaN | NaN | NaN | | 94,476 | 1 |
| NaN | NaN | NaN | NaN | NaN | 113.66 | | 1 |
| NaN | NaN | NaN | NaN | NaN | 101.06 | | 1 |
| -0.00012533 | -0.87695 | -0.00066937 | ########## | ########## | | 87,498 | 0.53297 |

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|---|---|---|---|---|---|---|---|
| 0.00066917 | NaN | NaN | NaN | NaN | | 57,495 | 0.41724 |
| -0.00012276 | -11,423 | -0.00072262 | ########## | ########## | | 53,759 | 0.55851 |
| 1.20E-02 | -0.55212 | -0.00034928 | ########## | ########## | | 63,476 | 0.71551 |
| 0.00036841 | NaN | NaN | NaN | NaN | 66.49 | | 0.72619 |
| 0.00040937 | NaN | NaN | NaN | NaN | | 57,738 | 0.36544 |
| -0.00032366 | -10,283 | -0.00065052 | ########## | ########## | | 55,677 | 0.57108 |

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|---|---|---|---|---|---|---|---|
| -0.0011037 | NaN | NaN | NaN | NaN | | 59,949 | 0.91953 |
| -0.00064366 | NaN | NaN | NaN | NaN | | 59,764 | 0.9465 |
| -0.00092598 | NaN | NaN | NaN | NaN | | 61,765 | 1,128 |
| -0.0012451 | NaN | NaN | NaN | NaN | 123.93 | | 0.76739 |

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|---|---|---|---|---|---|---|---|
| 2.77E-02 | -18,612 | -0.0016926 | ########## | ########## | | 88,764 | 0.6004 |
| -0.00072269 | -17,281 | -0.0010483 | ########## | ########## | | 89,718 | 14,088 |
| -0.00077341 | -13,769 | -0.00083528 | ########## | ########## | 89.86 | | 11,759 |
| -0.0006508 | -14,476 | -0.00087818 | ########## | ########## | | 89,509 | 0.76118 |
| -0.00051312 | -11,403 | -0.00068147 | ########## | ########## | | 68,206 | 19,744 |

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|---|---|---|---|---|---|---|---|
| -0.0015969 | -20,596 | -0.0018453 | ########## | ########## | | 74,517 | 0.44894 |
| -0.00045077 | -1,625 | -0.0014559 | ########## | ########## | | 74,981 | 0.66922 |
| -0.00016479 | -0.92031 | -0.00055 | ########## | ########## | | 67,525 | 0.73146 |

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|---|---|---|---|---|---|---|---|
| 0.00043523 | NaN | NaN | NaN | NaN | | 86,999 | 0.7193 |
| 0.0011086 | NaN | NaN | NaN | NaN | | 85,962 | 0.63573 |
| 0.0015461 | NaN | NaN | NaN | NaN | | 84,968 | 0.63683 |
| 5.53E-02 | NaN | NaN | NaN | NaN | | 82,974 | 0.69716 |
| 0.0012608 | NaN | NaN | NaN | NaN | | 84,321 | 0.64992 |
| 0.001306 | NaN | NaN | NaN | NaN | 83.74 | | 0.96486 |

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|---|---|---|---|---|---|---|---|
| -0.00033326 | NaN | NaN | NaN | NaN | | 95,998 | 0.73493 |
| 0.00037473 | NaN | NaN | NaN | NaN | | 105 | 0.64604 |
| -0.00036333 | -10,028 | -0.00091697 | ########## | ########## | | 95,819 | 0.87028 |

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|---|---|---|---|---|---|---|---|
| -0.00021767 | -10,359 | -0.00057521 | ########## | ########## | | 55,913 | 0.41409 |
| -0.00025435 | -12,069 | -0.0010046 | ########## | ########## | | 57,181 | 0.44668 |
| -0.00013829 | -0.43849 | -0.00024348 | ########## | ########## | | 65,694 | 0.53619 |
| 0.000444 | -0.16528 | -0.00013758 | ########## | ########## | | 64,475 | 0.49722 |
| -8.28E-01 | -0.8866 | -0.00073801 | ########## | ########## | | 65,717 | 0.48075 |
| -0.0007084 | -16,961 | -0.0010142 | ########## | ########## | | 46,122 | 0.3931 |
| -0.00079715 | -17,929 | -0.0010721 | ########## | ########## | | 52,587 | 0.64492 |

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|---|---|---|---|---|---|---|---|
| 0.00044906 | -0.69823 | -0.00052669 | ########## | ########## | | 71,015 | 0.46674 |
| 0.00033729 | -0.23648 | -0.00017839 | ########## | ########## | | 69,722 | 0.74473 |
| 1.45E-01 | -0.67934 | -0.00051245 | ########## | ########## | | 81,242 | 0.67423 |

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|---|---|---|---|---|---|---|---|
| 0.00033928 | 0.17765 | 9.92E-01 | ########## | ########## | | 46,373 | 13,627 |
| 0.00058073 | NaN | NaN | NaN | NaN | | 48,931 | 0.67912 |

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|---|---|---|---|---|---|---|---|
| 0.0013452 | 0.36076 | 0.00034578 | ########## | ########## | 130.53 | | 1,487 |
| 0.00099024 | 0.89689 | 0.00085964 | ########## | ########## | | 132 | 15,108 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| -0.00078979 | -20,573 | -0.0012565 | ########## | ########## | 116.71 | | 0.92902 |
| -0.00089042 | -18,703 | -0.0011423 | ########## | ########## | | 46,818 | 0.65672 |
| -0.00071657 | -20,239 | -0.0012199 | ########## | ########## | 126.59 | | 17,975 |

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|---|---|---|---|---|---|---|---|
| -0.00010582 | NaN | NaN | NaN | NaN | | 73,446 | 0.85529 |
| -0.00034272 | NaN | NaN | NaN | NaN | | 71,689 | 0.95847 |
| -0.00046481 | NaN | NaN | NaN | NaN | | 68,475 | 0.57893 |
| -0.00013785 | NaN | NaN | NaN | NaN | | 63,488 | 0.81966 |
| -0.0001687 | NaN | NaN | NaN | NaN | 128.62 | | 23,097 |
| -0.0001651 | NaN | NaN | NaN | NaN | | 68,041 | 0.80257 |

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|---|---|---|---|---|---|---|---|
| -0.00069943 | NaN | | NaN | NaN | NaN | 66,515 | 11,619 |
| -0.00035497 | NaN | | NaN | NaN | NaN | 64,425 | 1,019 |
| -0.00058298 | NaN | | NaN | NaN | NaN | 121.77 | 39,073 |
| -0.00031859 | NaN | | NaN | NaN | NaN | 71,122 | 0.53815 |
| -0.00015354 | NaN | | NaN | NaN | NaN | 77,373 | 10,956 |
| -0.00028462 | NaN | | NaN | NaN | NaN | 75,968 | 12,429 |
| -0.00025744 | NaN | | NaN | NaN | NaN | 64,014 | 10,419 |
| -0.00070165 | NaN | | NaN | NaN | NaN | 118.8 | 25,957 |
| -0.00039808 | NaN | | NaN | NaN | NaN | 125.72 | 29,955 |
| -0.00060946 | NaN | | NaN | NaN | NaN | 129.27 | 2,961 |
| -0.0005495 | NaN | | NaN | NaN | NaN | 69.77 | 10,571 |
| -0.00026694 | NaN | | NaN | NaN | NaN | 63,333 | 0.77888 |

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|---|---|---|---|---|---|---|---|
| 0.00076401 | NaN | | NaN | NaN | NaN | 54,759 | 0.54944 |
| 0.00069075 | NaN | | NaN | NaN | NaN | 52,031 | 0.43327 |
| -0.0004052 | | -13,824 | -0.00099161 | ########## | ########## | 62,327 | 11,715 |
| -0.00026473 | | -15,564 | -0.0011164 | ########## | ########## | 56,364 | 0.55442 |
| 0.00059057 | NaN | | NaN | NaN | NaN | 52,195 | 0.50599 |
| -0.00030797 | | -13,206 | -0.00094725 | ########## | ########## | 51,827 | 0.88256 |
| -0.00034486 | | -14,158 | -0.0010155 | ########## | ########## | 52,567 | 0.85705 |
| 0.00044003 | NaN | | NaN | NaN | NaN | 50.78 | 0.51909 |

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|---|---|---|---|---|---|---|
| 0.0011183 | 0.98959 | 0.00098016 | ########## | ########## | 130.2 | 14,043 |
| 0.0016944 | 0.82589 | 0.00081803 | ########## | ########## | 101.65 | 2,687 |
| 0.0014991 | 0.79621 | 0.00078863 | ########## | ########## | 102.56 | 18,499 |
| 0.0010097 | 0.22998 | 0.00022779 | ########## | ########## | 102.36 | 0.76945 |
| 0.0015818 | 0.81593 | 0.00080816 | ########## | ########## | 102.16 | 0.55981 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.0010802 | NaN | NaN | NaN | NaN | 81,284 | 13,858 |
| 0.0012056 | NaN | NaN | NaN | NaN | 81,377 | 16,813 |
| 6.89E-01 | NaN | NaN | NaN | NaN | 81,158 | 0.85651 |

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|---|---|---|---|---|---|---|
| 0.00030001 | NaN | NaN | NaN | NaN | 111.95 | 0.94267 |
| 0.00051464 | NaN | NaN | NaN | NaN | 114.19 | 0.63842 |
| 0.00071529 | NaN | NaN | NaN | NaN | 123.38 | 0.5867 |

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|---|---|---|---|---|---|---|
| -0.00095371 | -27,147 | -0.0018197 | ########## | ########## | 63,084 | 0.72208 |
| -0.001608 | -33,195 | -0.0022251 | ########## | ########## | 66.67 | 0.38632 |
| -0.0014848 | -30,196 | -0.0020241 | ########## | ########## | 64,794 | 0.56033 |

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|---|---|---|---|---|---|---|
| 0.00049439 | NaN | NaN | NaN | NaN | 42,096 | 0.57529 |
| -0.00060678 | -15,885 | -0.00086696 | ########## | ########## | 50,042 | 0.65393 |
| -0.00020773 | -17,386 | -0.0012645 | ########## | ########## | 42,335 | 0.72315 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.00055042 | NaN | NaN | NaN | NaN | 42,336 | 0.93044 |
| 0.00028094 | NaN | NaN | NaN | NaN | 43,609 | 10,889 |
| 0.00023955 | NaN | NaN | NaN | NaN | 50,433 | 0.32283 |
| -0.00019258 | -1.08 | -0.00078551 | ########## | ########## | 57,465 | 0.65966 |
| 0.00015941 | NaN | NaN | NaN | NaN | 57,517 | 0.85898 |
| 0.00049395 | NaN | NaN | NaN | NaN | 55,509 | 0.62685 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.00052278 | NaN | NaN | NaN | NaN | 54,745 | 0.51048 |
| -0.00075392 | -18,337 | -0.0013526 | ########## | ########## | 64,875 | 0.77584 |
| -0.00043785 | -13,261 | -0.00097824 | ########## | ########## | 53,482 | 0.68179 |
| 4.65E-01 | NaN | NaN | NaN | NaN | 106.88 | 10,294 |
| -0.00050752 | -13,644 | -0.0010065 | ########## | ########## | 52.9 | 0.56873 |

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|---|---|---|---|---|---|---|
| -0.00047885 | -11,911 | -0.0012256 | ########## | ########## | 120.16 | 12,281 |
| -0.0018201 | -17,689 | -0.0018201 | ########## | ########## | 119.81 | 11,799 |
| -0.0017367 | -16,878 | -0.0017367 | ########## | ########## | 119.92 | 1,068 |
| -0.0015987 | -15,537 | -0.0015987 | ########## | ########## | 119.98 | 0.58934 |
| -0.0010859 | -14,992 | -0.0015427 | ########## | ########## | 120.5 | 10,766 |
| 0.00041865 | NaN | NaN | NaN | NaN | 120.4 | 0.50204 |
| -0.0018155 | -17,644 | -0.0018155 | ########## | ########## | 120.97 | 0.6772 |
| -0.0016632 | -16,164 | -0.0016632 | ########## | ########## | 121.12 | 13,278 |
| -0.0011612 | -11,285 | -0.0011612 | ########## | ########## | 121.39 | 0.68147 |
| -0.0012866 | -14,072 | -0.001448 | ########## | ########## | 133.17 | 0.95207 |
| 0.0006433 | NaN | NaN | NaN | NaN | 133.21 | 0.64886 |
| -0.00041792 | -11,295 | -0.0011622 | ########## | ########## | 133.07 | 1,098 |
| -0.00049955 | -0.91365 | -0.00062705 | ########## | ########## | 133.09 | 0.57579 |
| 0.00012673 | NaN | NaN | NaN | NaN | 121.19 | 0.82292 |
| -0.00061214 | -14,789 | -0.0015217 | ########## | ########## | 121.83 | 0.82023 |
| 4.27E-01 | -0.82083 | -0.00056335 | ########## | ########## | 121.79 | 0.83508 |
| -0.0015071 | -14,647 | -0.0015071 | ########## | ########## | 121.84 | 0.78532 |
| -0.0014044 | -13,648 | -0.0014044 | ########## | ########## | 121.85 | 0.75122 |
| 2.52E-01 | NaN | NaN | NaN | NaN | 121.87 | 0.56217 |
| -7.30E-01 | NaN | NaN | NaN | NaN | 122.13 | 0.63235 |
| -0.00058993 | -0.69372 | -0.00071382 | ########## | ########## | 123.85 | 24,877 |
| 0.00011339 | -0.41096 | -0.00042286 | ########## | ########## | 121.54 | 0.76222 |
| -0.00060268 | -0.83917 | -0.00086349 | ########## | ########## | 120.81 | 0.62215 |
| -0.00013279 | -0.73465 | -0.00075593 | ########## | ########## | 121.92 | 18,693 |
| -0.00069648 | -0.67687 | -0.00069648 | ########## | ########## | 122.16 | 0.78681 |
| NaN | NaN | NaN | NaN | NaN | 122.13 | 1 |
| -0.00022238 | -0.21612 | -0.00022238 | ########## | ########## | 122.46 | 0.56194 |
| -0.0004762 | -11,352 | -0.0011681 | ########## | ########## | 120.15 | 0.95764 |

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|---|---|---|---|---|---|---|
| 0.00066326 | NaN | NaN | NaN | NaN | 82,514 | 0.82999 |

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|---|---|---|---|---|---|---|
| 0.00081082 | NaN | NaN | NaN | NaN | 83,068 | 0.49942 |
| -0.00062624 | -11,515 | -0.00079837 | ########## | ########## | 84,379 | 0.89329 |

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|---|---|---|---|---|---|---|
| 0.0016252 | NaN | NaN | NaN | NaN | 105.61 | 0.69661 |
| -0.00014368 | -0.89137 | -0.00073663 | ########## | ########## | 100.9 | 0.40081 |
| 0.001689 | NaN | NaN | NaN | NaN | 105.18 | 0.58349 |
| 0.00049251 | -0.30446 | -0.00025161 | ########## | ########## | 101.02 | 0.55649 |
| 0.00019225 | -0.37286 | -0.00030813 | ########## | ########## | 99,569 | 0.63045 |
| 0.00041986 | -0.12055 | -0.00010444 | ########## | ########## | 116.48 | 0.51491 |

| | | | | | | |
|---|---|---|---|---|---|---|
| -0.0011366 | -14,209 | -0.0011366 | ########## | ########## | 87,404 | 0.47132 |
| -0.00047887 | -0.59866 | -0.00047887 | ########## | ########## | 85,976 | 0.56593 |
| 5.25E-01 | -0.53997 | -0.00043193 | ########## | ########## | 85,818 | 0.46095 |
| -0.00053161 | -0.66459 | -0.00053161 | ########## | ########## | 85,572 | 0.62428 |

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|---|---|---|---|---|---|---|
| -0.00026598 | -0.80896 | -0.00035613 | ########## | ########## | 18,285 | 0.77988 |
| 0.00018816 | 0.14909 | 6.56E-01 | ########## | ########## | 23,095 | 0.53612 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.00082517 | NaN | NaN | NaN | NaN | 100.73 | 0.78802 |
| -0.00070433 | -0.89096 | -0.00089818 | ########## | ########## | 101.71 | 0.80127 |
| -0.00024359 | -0.93389 | -0.00094145 | ########## | ########## | 102.32 | 0.64181 |

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|---|---|---|---|---|---|---|
| -0.00041149 | NaN | NaN | NaN | NaN | 109.77 | 12,359 |
| 0.00048753 | NaN | NaN | NaN | NaN | 123.32 | 24,183 |
| 0.00069721 | NaN | NaN | NaN | NaN | 110.69 | 0.79527 |

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|---|---|---|---|---|---|---|
| 0.0011551 | Jan-67 | 0.0011217 | ########## | ########## | 136.58 | 0.83658 |
| 0.001285 | 19,226 | 0.0012914 | ########## | ########## | 123.02 | 49,787 |
| 0.00092914 | 16,331 | 0.0010969 | ########## | ########## | 130.28 | 13,125 |

| Calibrated retention time | Calibrated retention time start | Calibrated retention time finish | Retention time calibration | Match time difference | Match m/z difference | Match q-value |
|---|---|---|---|---|---|---|
| 88,682 | 88,396 | 89,005 | 15,086 | | | |
| 86,296 | 85.84 | 86,657 | 7,433 | | | |
| 82,298 | 82.03 | 82,611 | 15,086 | | | |
| 78,199 | 77,715 | 78,795 | 71,326 | | | |
| 73,611 | 73,316 | 73.89 | 15,086 | | | |
| 70,516 | 70,158 | 71,039 | 74,774 | | | |
| 78,238 | 78,026 | 78,608 | 15,086 | | | |
| 74.77 | 74,446 | 75,121 | 73,329 | | | |
| | | | | | | |
| 89,428 | 88,928 | 89,928 | 16,251 | | | |
| 89.57 | 89.07 | 90.07 | 16,153 | | | |
| | | | | | | |
| 104.38 | 104.12 | 104.7 | 0.96355 | | | |
| 104.58 | 104.14 | 104.99 | 4,162 | | | |
| 104.8 | 104.24 | 105.3 | 75,276 | | | |
| 103.74 | 103.3 | 105.28 | 13,625 | | | |
| 104.52 | 104.19 | 104.84 | 7,082 | | | |
| 104.53 | 104.22 | 104.81 | 71,179 | | | |
| 104.52 | 103.97 | 105.3 | 20,194 | | | |
| 104.5 | 104.11 | 105.16 | 65,146 | | | |
| 104.15 | 103.85 | 104.58 | -11,905 | -0.2187 | 0.00029497 | NaN |
| 104.86 | 104.64 | 105.06 | 46,491 | -0.0084508 | -0.00093103 | NaN |
| 104.94 | 104.7 | 105.26 | 6,304 | 0.074542 | 0.00030615 | NaN |
| 105.27 | 104.99 | 105.47 | 72,397 | | | |
| | | | | | | |
| 135.39 | 135.12 | 135.75 | 19,095 | | | |
| 132.19 | 132.02 | 132.34 | 12,687 | | | |
| 134.08 | 133.79 | 134.27 | 74,366 | | | |
| 128.76 | 128.37 | 128.94 | -7,775 | | | |
| 100.99 | 100.72 | 101.37 | -15,894 | | | |
| 101.36 | 101.13 | 101.66 | -15,771 | 0.183 | -0.0006071 | NaN |
| 110.96 | 110.53 | 111.36 | -15,894 | | | |
| 111.02 | 110.62 | 111.24 | -15,894 | | | |
| | | | | | | |
| 85,153 | 84,797 | 85,467 | 5,324 | | | |
| 86,045 | 85,642 | 86,465 | 72,776 | | | |
| 88,198 | 87,942 | 88,546 | 11,064 | | | |
| 84,867 | 84,016 | 85,445 | 35,258 | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 86,894 | 86,285 | 87,312 | 87,342 | | | |
| | | | | | | |
| 100.91 | 100.66 | 101.26 | 19,196 | | | |
| 90,685 | 90,438 | 90,985 | 5,224 | | | |
| 91,882 | 91,522 | 92,181 | 71,776 | | | |
| 95,804 | 95,551 | 96,123 | 13,888 | | | |
| 95,855 | 95.55 | 96,152 | 12,818 | | | |
| 88,706 | 88,454 | 88,991 | 73,008 | | | |
| 100.46 | 100.21 | 100.71 | 52,721 | | | |
| 101.56 | 101.28 | 101.91 | 68,355 | | | |
| 97,518 | 97,303 | 97,853 | 15,387 | | | |
| 93,081 | 92.79 | 93,372 | 86,341 | | | |
| 95,115 | 94.78 | 95,383 | 11,906 | | | |
| 97,608 | 97,316 | 97,805 | 15,681 | 0.045101 | 0.00031363 | NaN |
| | | | | | | |
| 83,294 | 82,811 | 84,379 | 65,389 | | | |
| 74,634 | 74,321 | 75,054 | -15,717 | | | |
| 92,495 | 92,273 | 92,774 | 15,908 | | | |
| 81,551 | 81,135 | 82,523 | 40,333 | | | |
| 85,429 | 85,159 | 85,746 | Jul-71 | | | |
| 94.9 | 94,616 | 95,153 | 72,329 | | | |
| 96,211 | 95,907 | 96,559 | 84,453 | | | |
| 88,911 | 88.57 | 89,437 | 10,799 | | | |
| 93.44 | 93,001 | 94,676 | 16,985 | | | |
| 104.69 | 104.38 | 105.09 | 25,969 | | | |
| 96,344 | 96,047 | 96,686 | 84,784 | 0.066776 | -0.00027052 | NaN |
| | | | | | | |
| 96,434 | 96,099 | 96,776 | 15,562 | | | |
| 101.75 | 101.4 | 101.93 | 75,363 | | | |
| | | | | | | |
| 101.92 | 101.66 | 102.42 | -10,905 | | | |
| 102.87 | 102.55 | 103.27 | 10,635 | | | |
| 106.32 | 105.95 | 106.71 | 63,039 | | | |
| 106.6 | 106.18 | 107.26 | -43,689 | | | |
| 104.66 | 104.32 | 105.01 | 20,194 | | | |
| 106.06 | 105.76 | 106.44 | 46,915 | | | |
| | | | | | | |
| 58,484 | 58,195 | 58,792 | 74,781 | | | |
| 60.63 | 60,381 | 60,985 | 34,263 | | | |
| | | | | | | |
| | | | | | | |
| 89,573 | 89,404 | 89,773 | 11,064 | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 90,527 | 90.11 | | 90,874 | 32,259 | | |
| | 88,402 | | 88,072 | 88,666 | 86,341 | | |
| | 93,264 | | 92,876 | 93,689 | 51,308 | | |
| | 93,584 | | 93,163 | 93,855 | 49,337 | | |
| | 93,358 | | 92,951 | 93,838 | 45,084 | | |
| 84.35 | | | 84,065 | 84,594 | 13,861 | | |
| | 86,597 | | 86,306 | 86,935 | 15,052 | | |
| | 87,258 | | 86,975 | 87,622 | 16.64 | | |
| 127.03 | | 126.78 | | 127.37 | 18,882 | | |
| | 92,842 | | 92,689 | 93,133 | -16,152 | | |
| 127.99 | | 127.68 | | 128.23 | 19,151 | | |
| | 78,645 | 78.34 | | 78,979 | 12,223 | | |
| | 79,931 | | 79,545 | 80,457 | 15,308 | | |
| | 79,961 | | 79,545 | 80,457 | 15,308 | | |
| | 80,397 | | 80,116 | 80,734 | 15,809 | | |
| 104.01 | | 103.51 | | 104.51 | 95,334 | | |
| | 91,039 | | 90,539 | 91,539 | -22.62 | | |
| | 90,247 | | 89,747 | 90,747 | -10,808 | | |
| | 93,917 | | 93,654 | 94,187 | 64,188 | | |
| | 64,873 | | 64,649 | 65,066 | 73,776 | | |
| | 70,036 | 69.74 | | 70,298 | 16,277 | | |
| 71.41 | | | 70,984 | 71.7 | 79,337 | | |
| | 67,525 | 67.14 | | 67,866 | 10,349 | | |
| | 70,505 | | 70,325 | 70.69 | 12,767 | | |
| | 67,784 | | 67,514 | 68,086 | 12,107 | | |
| | 74,601 | | 74,277 | 75,196 | 14,652 | | |
| 74.91 | | | 74,549 | 75,496 | 15,146 | | |
| | 74,532 | | 74,252 | 75.38 | 12,766 | | |
| 104.46 | | 104.26 | | 105.03 | -19,476 | | |
| | 92,904 | | 92,636 | 93,236 | 41,393 | | |
| | 94,746 | | 94,091 | 95.5 | 50,272 | | |
| | 94,791 | | 94,313 | 95,489 | 49,305 | -0.041153 | -0.00017331 NaN |
| | 94,959 | | 94,602 | 95,363 | 54,503 | 0.12724 | 0.00019452 NaN |
| | 82,757 | | 81,481 | 83,455 | 14,552 | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 89,364 | 89,119 | 89,568 | 14,847 | | | |
| | 89,433 | 89,182 | 89,851 | 14,452 | 0.034115 | 0.00081033 | NaN |
| | 82,596 | 82,258 | 82.99 | 15,072 | -0.024422 | 0.00039573 | NaN |
| | | | | | | | |
| 101.78 | | 101.32 | 102.04 | 14,786 | | | |
| 102.39 | | 102.07 | 102.71 | 16,433 | | | |
| 102.64 | | 102.25 | 102.89 | 17,669 | | | |
| | 89,947 | 89,633 | 90.33 | 69,729 | | | |
| 102.68 | | 102.23 | 102.88 | 18,364 | | | |
| 102.6 | | 102.23 | 103.19 | 18,858 | | | |
| | | | | | | | |
| | 89,819 | 89,454 | 90,189 | -61,797 | | | |
| 106.31 | | 106.07 | 106.72 | 1,319 | | | |
| 102.66 | | 102.21 | 103.08 | 68,448 | | | |
| | | | | | | | |
| | 70,999 | 70,781 | 71,195 | 15,086 | | | |
| | 69,999 | 69.77 | 70,217 | 12,818 | | | |
| | 66,729 | 66,453 | 66,989 | 10,349 | | | |
| | 67,301 | 67,076 | 67,574 | 28,262 | | | |
| | 66,751 | 66,453 | 66,934 | 10,349 | -0.27472 | -0.00060714 | NaN |
| | 61,208 | 61,025 | 61,419 | 15,086 | | | |
| | 60,065 | 59,868 | 60,513 | 74,781 | | | |
| | | | | | | | |
| | 82,279 | 82,057 | 82,523 | 11,264 | | | |
| 82.54 | | 82,217 | 82,961 | 12,818 | | | |
| | 83,176 | 82,873 | 83,547 | 19,343 | | | |
| | | | | | | | |
| 61.82 | | 61,491 | 62,854 | 15,446 | | | |
| | 64,376 | 63,856 | 64,536 | 15,445 | | | |
| | | | | | | | |
| 132.31 | | 131.6 | 133.09 | 17,792 | | | |
| 138.47 | | 137.36 | 138.88 | 64,748 | | | |
| | | | | | | | |
| 125.7 | | 125.43 | 126.36 | 89,881 | | | |
| | 62,572 | 62,327 | 62,984 | 15,754 | | | |
| 110.3 | | 109.5 | 111.29 | -16,286 | | | |
| | | | | | | | |
| 79.07 | | 78,797 | 79,652 | 5,624 | | | |
| | 79,267 | 78,869 | 79,828 | 75,776 | | | |
| | 79,353 | 79,035 | 79,614 | 10,877 | | | |
| | 79,841 | 79,541 | 80,361 | 16,353 | | | |
| 137.41 | | 136.35 | 138.66 | Aug-79 | | | |
| | 79,605 | 79,349 | 80,152 | 11,564 | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 79,533 | 79.2 | | 80,362 | 13,018 | | |
| | 79,571 | | 79,233 | 80,252 | 15,146 | | |
| 117.36 | | 115.3 | | 119.21 | -4.41 | | |
| | 78,254 | | 78,052 | 78.59 | | 71,326 | |
| | 78,607 | | 78,338 | | 79,434 | 12,349 | |
| | 78,795 | | 78,468 | | 79,711 | 28,264 | |
| | 79,322 | | 78,967 | | 80,009 | 15,308 | |
| 117.33 | | 115.93 | | 118.52 | | -1,474 | |
| 117.94 | | 116.54 | | 119.54 | | -7,775 | |
| 112.99 | | 111.61 | | 114.57 | | -16,286 | |
| | 78,905 | | 78,599 | | 79,657 | 91,348 | |
| | 79,142 | | 78,859 | | 79,638 | 15,809 | |
| | 65,937 | 65.78 | | 66,329 | 11,178 | | |
| | 68,308 | 68.1 | | 68,534 | 16,277 | | |
| | 70,805 | | 70,492 | | 71,663 | 84,783 | |
| | 69,031 | | 68,797 | | 69,352 | 12,667 | |
| | 67,748 | | 67,541 | | 68,047 | 15,553 | |
| | 67,992 | | 67,722 | | 68,604 | 16,165 | |
| | 67,095 | | 66,778 | | 67,635 | 14,528 | |
| | 68,119 | | 67,908 | | 68,427 | 17,339 | |
| 127.38 | | 126.72 | | 128.13 | | -28,205 | |
| | 91,871 | | 91,424 | | 94,111 | -97,767 | |
| | 91,754 | | 91,367 | | 93,217 | -10,805 | |
| | 91,648 | | 91,276 | | 92,046 | -10,707 | -0.045914 -0.00071351 NaN |
| 91.68 | | | 91,441 | | 92 | -10,484 | -0.014114 0.0004307 NaN |
| | 95,931 | | 95,438 | | 96,824 | 14,647 | |
| | 95,986 | | 95,643 | | 97,325 | 14,609 | |
| | 96,007 | 95.73 | | | 96,587 | 14,849 | |
| 131.04 | | 130.73 | | 131.67 | | 19,095 | |
| 130.72 | | 130.46 | | 131.1 | | 16,528 | |
| 130.23 | | 129.91 | | 130.5 | | 68,524 | |
| | 77,736 | | 77,388 | 78.11 | | 14,652 | |
| | 78,233 | 78.05 | | | 78,437 | 11,564 | 0.30605 -0.00075337 NaN |
| | 77,812 | | 77,542 | | 78,103 | 13,018 | -0.11486 -0.00038386 NaN |
| | 58,848 | | 58,649 | | 59,224 | 16,752 | |
| | 57,547 | 57.25 | | | 57,904 | 75,053 | |
| 59.31 | | | 58,947 | 59.67 | | 16,975 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 59,312 | 58,829 | 59.76 | | 16,975 | | |
| 58,862 | 58,414 | 59,503 | | 15,253 | | |
| 58,767 | 58,553 | 58,876 | | 83,342 | | |
| 59 | 58,688 | 59,348 | | 15,351 | | |
| 59,052 | 58,547 | 59,406 | | 15,351 | | |
| 58,935 | 58,636 | 59,263 | | 34,263 | | |
| | | | | | | |
| 66,968 | 66.75 | | 67,261 | 12,223 | | |
| 67,702 | 67,352 | 68,128 | | 28,262 | | |
| 68,789 | 68,474 | 69,156 | | 15,308 | | |
| 99,005 | 98,655 | 99,685 | | -78,752 | | |
| 69,009 | 68,747 | 69,316 | | 16,109 | | |
| | | | | | | |
| 134.91 | 134.46 | 135.69 | | 14,748 | | |
| 95,223 | 94,798 | 95,978 | | -24,592 | | |
| 95,257 | 94,854 | 95,922 | | -24,667 | | |
| 96,836 | 96,597 | 97,186 | | -23,143 | | |
| 134.77 | 134.35 | 135.43 | | 14,277 | | |
| 132.85 | 132.62 | 133.12 | | 12,449 | | |
| 101.21 | 100.93 | 101.61 | | -19,762 | | |
| 101.57 | 101.1 | 102.43 | | -19,551 | | |
| 101.9 | 101.6 | 102.28 | -19.49 | | | |
| 140.2 | 139.77 | 140.72 | | 70,318 | | |
| 140.24 | 139.96 | 140.6 | | 70,318 | | |
| 139.44 | 139 | 140.1 | | 63,746 | | |
| 139.46 | 139.14 | 139.72 | | 63,746 | | |
| 133.04 | 132.66 | 133.48 | | 11,854 | | |
| 106.04 | 105.62 | 106.44 | | -15,786 | | |
| 106.01 | 105.69 | 106.53 | | -15,786 | | |
| 105.47 | 105.17 | 105.96 | -16.37 | | | |
| 110.64 | 110.29 | 111.05 | | -11,217 | | |
| 110.65 | 110.38 | 110.95 | | -11,217 | | |
| 107.67 | 107.41 | 108.04 | | -14,454 | | |
| 116.08 | 115.68 | 118.17 | | -7,775 | | |
| 133.51 | 133.11 | 133.87 | | 11,971 | | |
| 131.31 | 131.05 | 131.67 | | 10,506 | | |
| 106.02 | 105.52 | 107.39 | | -15,894 | | |
| 102.68 | 102.32 | 103.11 | | -19,482 | | |
| 102.65 | 102.15 | 103.15 | | -19,482 | | |
| 119.33 | 119.06 | 119.62 | | -31,306 | | |
| 134.43 | 134.07 | 135.03 | | 14,285 | -0.2373 | 2.57E-02 NaN |
| | | | | | | |
| 74,493 | 74,168 | 74,998 | | -80,209 | | |

| | | | | |
|---|---|---|---|---|
| 103.13 | 102.89 | 103.39 | 20,062 | |
| 95,077 | 94,701 | 95,594 | 10,699 | |
| | | | | |
| 106.57 | 106.13 | 106.83 | 0.96355 | |
| 89,438 | 89,273 | 89,673 | -11,459 | |
| 107.2 | 106.99 | 107.57 | 20,194 | |
| 90,677 | 90,413 | 90,969 | -10,344 | |
| 106.41 | 106.01 | 106.64 | 68,448 | |
| 100.59 | 100.37 | 100.88 | -15,894 | |
| | | | | |
| 93,802 | 93.59 | 94,061 | 6,398 | |
| 93,687 | 93,465 | 94,031 | 77,113 | |
| 90,358 | 90,157 | 90,618 | 45,403 | |
| 92,529 | 92,252 | 92,877 | 69,571 | |
| | | | | |
| 35,537 | 35.11 | 35.89 | 17,251 | |
| 33,624 | 33,368 | 33,904 | 10,529 | |
| | | | | |
| 91.62 | 91,221 | 92,009 | -91,056 | |
| 90,709 | 90,255 | 91,056 | -11 | |
| 90,794 | 90,466 | 91,107 | -11,525 | |
| | | | | |
| 129.53 | 129.05 | 130.29 | 19,759 | |
| 134.2 | 132.87 | 135.29 | 10,886 | |
| 128.26 | 127.84 | 128.64 | 17,564 | |
| | | | | |
| 133.66 | 133.44 | 134.27 | -29,207 | |
| 137.09 | 135.07 | 140.05 | 14,078 | |
| 137.31 | 136.42 | 137.73 | 70,318 | |

| Match score | Number of data points | Number of scans | Number of isotopic peaks | PIF | Fraction of total spectrum | Base peak fraction |
|---|---|---|---|---|---|---|
| | 51 | 13 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | | | |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 54 | 7 | 12 | 0 | 0 | 0 |
| | 74 | 11 | 12 | 0 | 0 | 0 |
| | 79 | 13 | 13 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 89 | 9 | 14 | 0 | 0 | 0 |
| | 49 | 8 | 10 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 91 | 14 | 13 | 0 | 0 | 0 |
| 76,533 | 72 | 12 | 13 | NaN | NaN | NaN |
| 87,352 | 152 | 21 | 11 | NaN | NaN | NaN |
| 87,352 | 75 | 13 | 11 | NaN | NaN | NaN |
| | | | | 0 | 0 | 0 |
| | 138 | 22 | 12 | 0 | 0 | 0 |
| | 96 | 21 | 6 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 42 | 7 | 10 | 0 | 0 | 0 |
| | 338 | 43 | 11 | 0 | 0 | 0 |
| 63,883 | 203 | 35 | 9 | NaN | NaN | NaN |
| | 337 | 55 | 9 | 0 | 0 | 0 |
| | 171 | 41 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 102 | 14 | 16 | 0 | 0 | 0 |
| | 128 | 23 | 9 | 0 | 0 | 0 |
| | 40 | 7 | 9 | 0 | 0 | 0 |
| | 40 | 8 | 8 | 0 | 0 | 0 |
| | 248 | 38 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 33 | 6 | 9 | 0 | 0 | 0 |
| | 49 | 8 | 10 | 0 | 0 | 0 |
| | 228 | 36 | 9 | 0 | 0 | 0 |
| | 44 | 7 | 9 | 0 | 0 | 0 |
| | 61 | 8 | 10 | 0 | 0 | 0 |
| 101.23 | 153 | 33 | 8 | NaN | NaN | NaN |
| | 633 | 102 | 9 | 0 | 0 | 0 |
| | 252 | 48 | 8 | 0 | 0 | 0 |
| | 135 | 33 | 6 | 0 | 0 | 0 |
| | 539 | 91 | 9 | 0 | 0 | 0 |
| | 167 | 39 | 6 | 0 | 0 | 0 |
| | 72 | 17 | 6 | 0 | 0 | 0 |
| | 61 | 16 | 7 | 0 | 0 | 0 |
| | 218 | 57 | 6 | 0 | 0 | 0 |
| | 594 | 111 | 9 | 0 | 0 | 0 |
| | 221 | 48 | 7 | 0 | 0 | 0 |
| 48,532 | 25 | 8 | 5 | NaN | NaN | NaN |
| | 36 | 8 | 6 | 0 | 0 | 0 |
| | 21 | 6 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 45 | 9 | 7 | 0 | 0 | 0 |
| | 240 | 32 | 12 | 0 | 0 | 0 |
| | 109 | 14 | 13 | 0 | 0 | 0 |
| | 76 | 11 | 11 | 0 | 0 | 0 |
| | 297 | 33 | 12 | 0 | 0 | 0 |
| | 158 | 32 | 7 | 0 | 0 | 0 |
| | 103 | 22 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 |
| | 45 | 7 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 74 | 16 | 7 | 0 | 0 | 0 |
| | 39 | 14 | 5 | 0 | 0 | 0 |
| | 149 | 34 | 8 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 190 | 32 | 10 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 124 | 13 | 15 | 0 | 0 | 0 |
| | 114 | 13 | 13 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 73 | 15 | 7 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 120 | 28 | 7 | 0 | 0 | 0 |
| | 88 | 33 | 6 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 208 | 31 | 10 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 62 | 11 | 8 | 0 | 0 | 0 |
| | 170 | 23 | 11 | 0 | 0 | 0 |
| 41,621 | 115 | 15 | 10 | NaN | NaN | NaN |
| 41,621 | 127 | 25 | 9 | NaN | NaN | NaN |
| | 194 | 28 | 10 | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 38 | 7 | 7 | 0 | 0 | 0 |
| 43.69 | 49 | 8 | 10 | NaN | NaN | NaN |
| 44,246 | 164 | 38 | 7 | NaN | NaN | NaN |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 488 | 58 | 12 | 0 | 0 | 0 |
| | 138 | 25 | 8 | 0 | 0 | 0 |
| | 44 | 9 | 8 | 0 | 0 | 0 |
| | 42 | 12 | 6 | 0 | 0 | 0 |
| | 24 | 6 | 6 | 0 | 0 | 0 |
| 72,316 | 32 | 10 | 7 | NaN | NaN | NaN |
| | 163 | 24 | 9 | 0 | 0 | 0 |
| | 160 | 30 | 11 | 0 | 0 | 0 |
| | 104 | 21 | 9 | 0 | 0 | 0 |
| | 42 | 10 | 8 | 0 | 0 | 0 |
| | 50 | 8 | 10 | 0 | 0 | 0 |
| | 497 | 80 | 15 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 701 | 98 | 10 | 0 | 0 | 0 |
| | 157 | 20 | 9 | 0 | 0 | 0 |
| | 58 | 14 | 8 | 0 | 0 | 0 |
| | 179 | 40 | 6 | 0 | 0 | 0 |
| | 173 | 77 | 4 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
| | 67 | 16 | 11 | 0 | 0 | 0 | |
| | 56 | 7 | 12 | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |
| | 239 | 30 | 12 | 0 | 0 | 0 | |
| | 346 | 40 | 12 | 0 | 0 | 0 | |
| | | | | 0 | 0 | 0 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 136 | 20 | 10 | 0 | 0 | 0 | |
| | 301 | 34 | 14 | 0 | 0 | 0 | |
| | 196 | 26 | 16 | 0 | 0 | 0 | |
| 47,622 | 217 | 25 | 13 | NaN | NaN | NaN | |
| 47,622 | 219 | 30 | 12 | NaN | NaN | NaN | |

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|---|---|---|---|---|---|---|
| | | | 0 | 0 | 0 | |
| | | | 0 | 0 | 0 | |
| | | | 0 | 0 | 0 | |

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|---|---|---|---|---|---|---|
| | | | 0 | 0 | 0 | |
| | | | 0 | 0 | 0 | |
| | | | 0 | 0 | 0 | |

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|---|---|---|---|---|---|---|---|
| | 66 | 11 | 10 | 0 | 0 | 0 | |
| 43,115 | 123 | 24 | 8 | NaN | NaN | NaN | |
| 43,115 | 45 | 8 | 9 | NaN | NaN | NaN | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | 0 | 0 | 0 | |
| | 287 | 34 | 12 | 0 | 0 | 0 | |
| | 161 | 32 | 8 | 0 | 0 | 0 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 79 | 25 | 5 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |

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|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 |
| | 86 | 10 | 13 | 0 | 0 | 0 |
| | 61 | 10 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 235 | 30 | 12 | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 130 | 15 | 14 | 0 | 0 | 0 |
| | 752 | 79 | 15 | 0 | 0 | 0 |
| | 709 | 71 | 15 | 0 | 0 | 0 |
| | 190 | 39 | 8 | 0 | 0 | 0 |
| | 130 | 13 | 14 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 282 | 45 | 10 | 0 | 0 | 0 |
| | 865 | 89 | 14 | 0 | 0 | 0 |
| | 211 | 45 | 7 | 0 | 0 | 0 |
| | 135 | 15 | 13 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 109 | 15 | 13 | 0 | 0 | 0 |
| | 41 | 7 | 9 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 442 | 54 | 12 | 0 | 0 | 0 |
| | 170 | 55 | 6 | 0 | 0 | 0 |
| | 421 | 52 | 11 | 0 | 0 | 0 |
| | 428 | 50 | 11 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 834 | 147 | 10 | 0 | 0 | 0 |
| | 48 | 9 | 8 | 0 | 0 | 0 |
| | 214 | 42 | 8 | 0 | 0 | 0 |
| | 1043 | 126 | 15 | 0 | 0 | 0 |
| | 391 | 55 | 10 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 |
| | 194 | 38 | 8 | 0 | 0 | 0 |
| 128.33 | 556 | 63 | 12 | NaN | NaN | NaN |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | 0 | 0 | 0 |

| | | | | | |
|---|---|---|---|---|---|
| | | | 0 | 0 | 0 |
| 342 | 59 | 9 | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| 88 | 27 | 5 | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| 81 | 21 | 7 | 0 | 0 | 0 |
| 154 | 42 | 7 | 0 | 0 | 0 |
| 132 | 34 | 5 | 0 | 0 | 0 |
| 172 | 31 | 9 | 0 | 0 | 0 |
| 147 | 37 | 7 | 0 | 0 | 0 |
| 152 | 30 | 7 | 0 | 0 | 0 |
| 255 | 41 | 9 | 0 | 0 | 0 |
| 258 | 50 | 7 | 0 | 0 | 0 |
| 112 | 37 | 6 | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| 92 | 10 | 13 | 0 | 0 | 0 |
| 76 | 10 | 11 | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| | | | 0 | 0 | 0 |
| 93 | 12 | 15 | 0 | 0 | 0 |
| 510 | 76 | 10 | 0 | 0 | 0 |
| 72 | 17 | 7 | 0 | 0 | 0 |

| PEP | MS/MS Count | MS/MS Scan Number | Score | Delta score | Combinatorics | Ratio H/L |
|---|---|---|---|---|---|---|
| 0.0024998 | 1 | 8758 | 50,873 | 36,926 | 10 | 0.32364 |
| 0.00066166 | 2 | 9811 | 63,937 | 45,532 | 10 | 0.39827 |
| 0.011114 | 1 | 7485 | 56.48 | 27,381 | 5 | 0.189 |
| 0.015999 | 1 | 8380 | 54,047 | 32,371 | 5 | 0.27281 |
| 0.013065 | 1 | 5937 | 41,615 | 26,992 | 5 | 0.25025 |
| 0.0012876 | 1 | 6660 | 53,625 | 31,949 | 5 | 0.14797 |
| 0.00037934 | 1 | 6747 | 55,302 | 26,579 | 10 | 0.2281 |
| 0.0045661 | 1 | 7721 | 42,209 | 20,086 | 10 | 0.37424 |
| | | | | | | |
| 0.02807 | 1 | 10887 | 45,433 | 82,528 | 1 | |
| 0.014498 | 1 | 7441 | 57,149 | 22.38 | 1 | |
| | | | | | | |
| 0.0025375 | 3 | 15318 | 67,396 | 61,087 | 2 | 0.54438 |
| 0.0010496 | 2 | 15421 | 76,533 | 55,254 | 2 | 0.49769 |
| 9.88E-01 | 1 | 15234 | 87,352 | 62,871 | 2 | 0.49671 |
| 0.0093801 | 1 | 17999 | 56.48 | 28,389 | 2 | 0.34323 |
| 0.0030875 | 1 | 15853 | 58,796 | 39,861 | 2 | 0.49439 |
| 2.20E-11 | 1 | 15878 | 118.67 | 103.82 | 2 | 11,087 |
| 0.011985 | 1 | 14078 | 54.15 | 28,274 | 2 | 0.16628 |
| 1.39E-03 | 1 | 14879 | 99,409 | 80,404 | 2 | 0.46245 |
| NaN | 0 | | NaN | NaN | 0 | 0.55402 |
| NaN | 0 | | NaN | NaN | 0 | 12,755 |
| NaN | 0 | | NaN | NaN | 0 | 0.57747 |
| 0.022911 | 1 | 16018 | 47,603 | 15.25 | 4 | 0.51852 |
| | | | | | | |
| 0.0096279 | 1 | 16802 | 83.31 | 83.31 | 5 | 0.62157 |
| 0.038931 | 1 | 18314 | 65,207 | 45,627 | 5 | 0.53203 |
| 0.02059 | 1 | 20557 | 96,391 | 63,022 | 5 | 0.43102 |
| 0.001369 | 1 | 12202 | 95,444 | 95,444 | 5 | 0.63294 |
| 0.044014 | 1 | 8067 | 63,883 | 44,861 | 5 | 0.59556 |
| NaN | 0 | | NaN | NaN | 0 | 0.43797 |
| 0.0004661 | 2 | 8847 | 90.78 | 72.2 | 10 | 0.51119 |
| 0.019791 | 1 | 8859 | 43,794 | 43,794 | 10 | 0.47973 |
| | | | | | | |
| 2.37E-03 | 1 | 9284 | 56,099 | 33,977 | 9 | 0.1246 |
| 5.44E-03 | 1 | 10051 | 51,264 | 31,511 | 9 | 0.081331 |
| 0.00031051 | 1 | 7891 | 42,301 | 20,735 | 9 | 0.12181 |
| 0.00078287 | 1 | 10748 | 40,129 | 24,923 | 9 | 0.18889 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.013428 | 1 | 8952 | 45,842 | 29,153 | 9 | NaN |
| | | | | | | |
| 0.00011047 | 1 | 10305 | 114.99 | 71,032 | 2 | 0.27122 |
| 0.021028 | 1 | 10475 | 90,755 | 46,157 | 2 | 0.41465 |
| 2.74E-02 | 1 | 11305 | 128.79 | 86,731 | 2 | 0.19931 |
| 0.0087381 | 1 | 5589 | 98,077 | 44,682 | 2 | 0.42649 |
| 0.00059842 | 1 | 12030 | 103.99 | 70,796 | 2 | 0.12084 |
| 0.0099793 | 1 | 5466 | 94,973 | 53,491 | 2 | 0.12082 |
| 1.62E-01 | 1 | 13652 | 131.54 | 84,649 | 2 | 0.38566 |
| 4.09E-01 | 1 | 13835 | 125.51 | 65,422 | 2 | 0.35571 |
| 0.005735 | 1 | 5602 | 101.23 | 78 | 2 | 0.62417 |
| 7.66E-09 | 1 | 10295 | 154.48 | 111.1 | 2 | 0.27884 |
| 6.83E-03 | 2 | 10693 | 139.74 | 84,787 | 2 | 0.47856 |
| NaN | 0 | | NaN | NaN | 0 | 0.21525 |
| | | | | | | |
| 0.0027448 | 3 | 5000 | 113.69 | 81,986 | 3 | 0.34725 |
| 0.0027173 | 1 | 5304 | 99,991 | 75,481 | 3 | 0.34253 |
| 0.022825 | 1 | 5646 | 64,313 | 50,913 | 3 | 0.74067 |
| 0.0024174 | 2 | 5047 | 112.42 | 75,976 | 3 | 0.31066 |
| 0.013363 | 1 | 5352 | 69,314 | 42,956 | 3 | 0.29144 |
| 0.012442 | 1 | 11571 | 70,438 | 43,549 | 3 | 0.62239 |
| 0.017913 | 1 | 12775 | 48,532 | 19,229 | 3 | 0.48128 |
| 0.0060641 | 1 | 5110 | 79,886 | 54,922 | 3 | 0.259 |
| 0.0034134 | 3 | 5036 | 91,307 | 61,303 | 3 | 0.29809 |
| 0.0036161 | 2 | 5500 | 86,803 | 58,598 | 3 | 0.2857 |
| NaN | 0 | | NaN | NaN | 0 | 0.46249 |
| | | | | | | |
| 0.0057169 | 1 | 14238 | 65,224 | 65,947 | 1 | 0.70699 |
| 0.013013 | 1 | 14612 | 54,066 | 15,763 | 1 | 0.3297 |
| | | | | | | |
| 0.026132 | 1 | 14173 | 64,346 | 42,864 | 2 | 0.17971 |
| 0.00017333 | 1 | 14967 | 91,414 | 66,183 | 2 | 0.24866 |
| 0.0012865 | 1 | 15524 | 72,793 | 53.63 | 2 | 0.11958 |
| 0.0024762 | 1 | 17094 | 66,777 | 66,777 | 2 | 0.19281 |
| 0.0046037 | 1 | 14113 | 60,938 | 60,938 | 2 | 0.39613 |
| 0.016277 | 1 | 14290 | 50,722 | 31,033 | 2 | 0.4492 |
| | | | | | | |
| 0.0066911 | 1 | 4389 | 47,039 | 15,317 | 2 | 0.37845 |
| 0.023679 | 1 | 5542 | 40,767 | 24,827 | 2 | 0.47176 |
| | | | | | | |
| | | | | | | |
| 0.0036427 | 1 | 8183 | 53,603 | 35,982 | 4 | NaN |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0037112 | 1 | 12115 | 53,444 | | 27,084 | 4 | 0.20669 |
| 0.0087212 | 1 | 9313 | 40,086 | | 22,324 | 4 | 0.32137 |
| 0.0053796 | 1 | 13274 | 55,588 | | 34,365 | 3 | 0.20466 |
| 0.005144 | 1 | 13684 | 55,846 | 32.21 | | 3 | 0.28266 |
| 0.0092671 | 1 | 12933 | 51,323 | | 30,538 | 3 | 0.41583 |
| 0.033384 | 1 | 7994 | 72,321 | | 24,037 | 2 | 31,103 |
| 0.018663 | 1 | 8978 | 62,166 | 15.76 | | 2 | 12,633 |
| 0.0037806 | 1 | 7516 | 80,632 | 50.02 | | 2 | 0.33563 |
| 0.01242 | 1 | 14018 | 46,099 | | 26-May | 2 | 0.43173 |
| 0.025403 | 1 | 7613 | 44,045 | | 15,496 | 2 | NaN |
| 0.0075169 | 1 | 14614 | 49,326 | | 27,441 | 2 | 0.4862 |
| 0.0062369 | 1 | 7138 | 42,863 | | 25,104 | 4 | 0.2213 |
| 1.63E-04 | 1 | 10094 | 80,664 | 58.9 | | 4 | NaN |
| 3.58E-04 | 1 | 10118 | 76,807 | | 57,114 | 4 | 0.26256 |
| 9.41E-01 | 1 | 6563 | 66,845 | 42.34 | | 4 | 0.2477 |
| 0.039708 | 1 | 12403 | 46,145 | | 20,121 | 1 | |
| 0.03181 | 1 | 17663 | 46,701 | | 20,706 | 1 | |
| 0.03593 | 1 | 15186 | 42,095 | | 26,854 | 1 | |
| 0.005205 | 1 | 10972 | 42,059 | | 31,197 | 2 | 0.37748 |
| 0.023872 | 1 | 5568 | 50,831 | | 30,601 | 3 | 0.41778 |
| 0.018293 | 1 | 6974 | 40,602 | | 27,181 | 3 | 0.5327 |
| 0.0056349 | 2 | 6932 | 48,711 | | 27,745 | 3 | 0.2539 |
| 0.018465 | 1 | 7406 | 54,004 | | 34,831 | 3 | 0.3153 |
| 0.0010818 | 1 | 6609 | 76,586 | | 54,589 | 3 | 0.3185 |
| 0.0024738 | 3 | 5136 | 56,121 | | 36,823 | 3 | 0.39543 |
| 0.0055099 | 1 | 7239 | 56,205 | | 11,358 | 3 | NaN |
| 0.020928 | 1 | 6553 | 40,242 | | 88,942 | 3 | NaN |
| 0.011604 | 1 | 7470 | 47,712 | | 97,173 | 3 | NaN |
| 0.0041436 | 1 | 9143 | 58,885 | | 23,208 | 3 | 10,111 |
| 0.014343 | 1 | 11748 | 44,252 | | 11,745 | 12 | 0.74268 |
| 0.0099871 | 1 | 12753 | 41,621 | | 41,621 | 12 | 0.64113 |
| NaN | 0 | NaN | NaN | | | 0 | 0.29793 |
| NaN | 0 | NaN | NaN | | | 0 | 0.83982 |
| 0.0093154 | 1 | 9040 | 44,246 | | 15,175 | 18 | 0.26957 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.035826 | 1 | 9568 | 43.69 | | 19,606 | 18 | 0.60977 |
| NaN | 0 | | NaN | NaN | | 0 | 0.26093 |
| NaN | 0 | | NaN | NaN | | 0 | 10,618 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0055019 | 1 | 12566 | 62,088 | | Dec-79 | 2 | 60,165 |
| 0.011075 | 1 | 11100 | 54,343 | | 26,289 | 2 | NaN |
| 0.0094476 | 1 | 10950 | 56,205 | 22.94 | | 2 | 14,999 |
| 0.013879 | 1 | 5804 | 51,135 | | 13,958 | 2 | 11,805 |
| 0.013592 | 1 | 12656 | 51,463 | | 18,198 | 2 | 7,004 |
| 0.028261 | 1 | 11531 | 43,798 | | 68,534 | 2 | NaN |

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|---|---|---|---|---|---|---|---|
| 0.00034151 | 1 | 6543 | 86,557 | | 67,693 | 4 | 0.14147 |
| 0.004696 | 1 | 15133 | 50,255 | | 26,363 | 4 | NaN |
| 0.0096204 | 1 | 6510 | 50,323 | | 22,645 | 4 | 0.35956 |

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|---|---|---|---|---|---|---|---|
| 0.011481 | 1 | 5455 | 44,468 | | 27,256 | 1 | 0.42219 |
| 0.011523 | 1 | 6599 | 64,749 | | 50,445 | 1 | 0.449 |
| 0.0026626 | 1 | 7257 | 55,575 | 38.65 | | 1 | 0.36541 |
| 0.0058585 | 1 | 7079 | 72,316 | | 72,316 | 1 | 0.39553 |
| NaN | 0 | | NaN | NaN | | 0 | 0.44217 |
| 0.004046 | 1 | 3914 | 43.05 | | 33.25 | 1 | 0.54788 |
| 0.0036301 | 1 | 4652 | 43,861 | | 35,553 | 1 | 0.41072 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0040337 | 1 | 6817 | 41,446 | | 19,745 | 1 | 0.22528 |
| 0.0010549 | 1 | 9182 | 50,178 | | 14,686 | 1 | 0.093787 |
| 0.0023183 | 1 | 10573 | 45,363 | | 26,499 | 1 | 0.34137 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0070692 | 1 | 4275 | 64,224 | | 81,371 | 2 | 0.21532 |
| 0.0026817 | 1 | 6598 | 75,416 | | 25,933 | 8 | 0.35198 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.032575 | 1 | 14601 | 47,537 | | 20,404 | 3 | 0.40559 |
| 0.040478 | 1 | 24658 | 43,861 | | 43,861 | 3 | 0.41982 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.010757 | 2 | 8200 | 51,949 | 37.48 | | 2 | 0.84105 |
| 0.022437 | 1 | 4435 | 41,427 | | 18,865 | 2 | 0.75432 |
| 0.041501 | 1 | 9477 | 45,022 | | 20,768 | 2 | 0.34812 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0182 | 1 | 7944 | 61,815 | | 21-Mar | 2 | NaN |
| 0.011692 | 1 | 8473 | 67,214 | | 18,266 | 2 | NaN |
| 0.011692 | 1 | 8462 | 67,214 | | 11,235 | 2 | 0.086717 |
| 0.041234 | 1 | 6118 | 51,998 | | 16,961 | 2 | NaN |
| 0.0052422 | 1 | 10100 | 76,927 | | 32,734 | 2 | 0.096784 |
| 0.0059889 | 1 | 6288 | 75,416 | | 26,118 | 2 | 0.01201 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0081995 | 1 | 8492 | 70,942 | 25,289 | 2 | 0.013381 | |
| 0.024685 | 1 | 7463 | 58,274 | 24,187 | 2 | 0.018572 | |
| 0.0017384 | 1 | 11862 | 90,827 | 56,827 | 2 | 0.21213 | |
| 0.038559 | 1 | 8382 | 53,013 | 68,068 | 2 | 0.044513 | |
| 0.018769 | 1 | 9720 | 61,344 | 10,335 | 2 | NaN | |
| 0.011692 | 1 | 9542 | 67,214 | 24,897 | 2 | 0.018412 | |
| 0.0059149 | 1 | 9958 | 75,566 | 35,693 | 2 | NaN | |
| 0.016684 | 1 | 9018 | 63,073 | 29,024 | 2 | 0.0723 | |
| 0.011855 | 2 | 10057 | 67.08 | 39,166 | 2 | 0.11481 | |
| 0.0076293 | 1 | 10005 | 72,096 | 31.62 | 2 | 0.047213 | |
| 0.0068534 | 1 | 7195 | 73,666 | 32,283 | 2 | 0.0062677 | |
| 0.031417 | 1 | 6332 | 55,721 | 20,953 | 2 | 0.024096 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.024113 | 1 | 5678 | 41,703 | 21,943 | 5 | NaN | |
| 0.0081741 | 1 | 6673 | 50,891 | 21,615 | 5 | NaN | |
| 0.00022932 | 2 | 9121 | 80,314 | 49,982 | 5 | 0.43213 | |
| 0.00015138 | 1 | 6309 | 89,043 | 56.69 | 5 | 0.68121 | |
| 0.0052321 | 1 | 5346 | 55,844 | 30,942 | 5 | 0.24467 | |
| 0.0011627 | 3 | 6431 | 60,761 | 37,535 | 5 | 0.61086 | |
| 0.00029277 | 2 | 5360 | 75,703 | 50,748 | 5 | 0.59265 | |
| 0.010752 | 1 | 4126 | 48,961 | 25,563 | 5 | 0.1266 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0044681 | 1 | 12023 | 49,066 | 20-Sep | 12 | 0.69795 | |
| 0.010474 | 1 | 16835 | 43,042 | 13,943 | 12 | 0.42738 | |
| 0.0050612 | 1 | 16316 | 47,622 | 13,729 | 12 | 0.4548 | |
| NaN | 0 | NaN | NaN | | 0 | 0.96313 | |
| NaN | 0 | NaN | NaN | | 0 | 0.65978 | |

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|---|---|---|---|---|---|---|---|
| 6.44E-02 | 1 | 11010 | 63,316 | 38,686 | 5 | 0.29767 | |
| 3.57E-04 | 2 | 13917 | 76,109 | 52,094 | 5 | 0.18027 | |
| 0.00044264 | 1 | 11006 | 49,912 | 30,606 | 5 | 0.27171 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.027894 | 1 | 16020 | 40,187 | 12,661 | 4 | 0.083061 | |
| 0.023762 | 1 | 17589 | 42,257 | 17,835 | 4 | NaN | |
| 0.0047553 | 1 | 19634 | 56,872 | 35,513 | 4 | 0.052186 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.014065 | 1 | 7899 | 43,115 | 65,234 | 6 | 0.5391 | |
| NaN | 0 | NaN | NaN | | 0 | 29,714 | |
| NaN | 0 | NaN | NaN | | 0 | 12,702 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.0090328 | 1 | 4505 | 84,436 | 56,117 | 3 | NaN | |
| 0.00050631 | 1 | 4212 | 54,004 | 54,004 | 3 | 0.66971 | |
| 0.00014728 | 2 | 4879 | 70,316 | 41,689 | 3 | 0.60681 | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.017538 | 1 | 4864 | 44,391 | 99,957 | 3 | 0.78079 |
| 0.0061945 | 1 | 4148 | 52,172 | 23,545 | 3 | 0.42382 |
| 0.020574 | 1 | 4797 | 42,708 | 20,468 | 3 | 0.49494 |
| 0.00013482 | 2 | 5616 | 71,376 | 52,796 | 3 | 0.84281 |
| 0.0070897 | 1 | 5597 | 50,376 | 31,796 | 3 | 0.45843 |
| 0.029933 | 1 | 5209 | 71,929 | 46,772 | 3 | 0.38952 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.026547 | 1 | 5129 | 44,029 | 24,268 | 3 | 0.15335 |
| 0.000655 | 1 | 7126 | 62,617 | 41,939 | 3 | 0.5177 |
| 0.016141 | 1 | 7635 | 42,639 | 22,609 | 3 | 0.35349 |
| 0.02124 | 1 | 7642 | 45,844 | 28,419 | 3 | NaN |
| 0.00062315 | 2 | 4701 | 56,748 | 39,862 | 3 | 0.63442 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 4.37E-16 | 3 | 21272 | 128.33 | 90,339 | 7 | 0.62808 |
| 0.00048003 | 1 | 8209 | 84,249 | 66,015 | 7 | 0.74161 |
| 2.01E-04 | 1 | 8303 | 107.75 | 90,506 | 7 | 0.63761 |
| 0.00048098 | 1 | 8283 | 84,208 | 84,208 | 7 | 0.58945 |
| 0.00045259 | 3 | 20748 | 85,423 | 46,147 | 7 | 0.55036 |
| 0.0034012 | 1 | 19553 | 56,719 | 35.15 | 7 | NaN |
| 0.0016868 | 2 | 8222 | 69,361 | 69,361 | 7 | 0.75594 |
| 6.03E-16 | 2 | 8373 | 125.73 | 108.49 | 7 | 0.56281 |
| 0.00039938 | 1 | 8323 | 87,228 | 65,659 | 7 | 0.50359 |
| 3.58E-03 | 3 | 21145 | 105.91 | 55,867 | 7 | 0.6626 |
| 0.0034179 | 1 | 21208 | 53,327 | 24.25 | 7 | 0.28191 |
| 9.33E-10 | 3 | 24871 | 122.6 | 93,847 | 7 | 0.66951 |
| 0.00050727 | 1 | 24926 | 69,612 | 46,275 | 7 | 0.80047 |
| 3.01E-07 | 2 | 21071 | 127.49 | 89,834 | 7 | 0.42587 |
| 0.00026142 | 3 | 9741 | 90,581 | 70,893 | 7 | 0.66297 |
| 0.0043172 | 1 | 9764 | 47,942 | 22,119 | 7 | 0.52528 |
| 0.00061323 | 4 | 8707 | 78,552 | 57,309 | 7 | 0.62127 |
| 0.00044057 | 5 | 8523 | 85,937 | 64,364 | 7 | 0.62092 |
| 0.0043557 | 2 | 8539 | 50,226 | 29.26 | 7 | 0.35126 |
| 0.00029721 | 2 | 8791 | 85,177 | 60,509 | 7 | 0.18401 |
| 4.64E-06 | 9 | 9905 | 115.56 | 89,013 | 7 | 0.50312 |
| 9.48E-01 | 1 | 21020 | 94,632 | 76,316 | 7 | 0.49387 |
| 0.00046045 | 1 | 16782 | 85,087 | 70,065 | 7 | 0.39694 |
| 1.12E-04 | 5 | 8495 | 111.3 | 72,495 | 7 | 0.50955 |
| 0.00020613 | 4 | 8376 | 91,926 | 74,207 | 7 | 0.50597 |
| 0.0076101 | 1 | 8395 | 58,864 | 30,698 | 7 | |
| 2.29E-01 | 1 | 8671 | 97,271 | 82,391 | 7 | 0.35501 |
| NaN | 0 | | NaN | NaN | 0 | 0.69868 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.020133 | 1 | 5593 | 41,257 | 18,627 | 6 | 0.25871 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 0.016457 | 1 | 8863 | 43,091 | 25,076 | 6 | NaN |
| 0.0021378 | 1 | 5542 | 50,358 | 21,809 | 6 | 0.46976 |
| 0.030294 | 1 | 15787 | 88,283 | 41,486 | 3 | 0.17475 |
| 0.021733 | 2 | 7087 | 90,385 | 63,123 | 3 | 0.27006 |
| 0.035888 | 1 | 14615 | 87,676 | 60,413 | 3 | 0.24707 |
| 0.0061697 | 1 | 13851 | 100.77 | 84,926 | 3 | 0.8397 |
| 0.0022498 | 1 | 6811 | 104.88 | 89,939 | 3 | 0.30248 |
| 0.0065927 | 1 | 8043 | 69,581 | 69,581 | 3 | 0.27591 |
| 8.66E-01 | 1 | 5983 | 106.31 | 85,721 | 3 | 0.96199 |
| 1.87E-01 | 1 | 5785 | 113.86 | 97,118 | 3 | 0.26731 |
| 0.0017519 | 1 | 5830 | 89,913 | 69,677 | 3 | 0.38826 |
| 0.0023236 | 2 | 5682 | 85,046 | 67,418 | 3 | 0.50712 |
| 0.011627 | 1 | 1240 | 42,629 | 30,571 | 4 | 0.58787 |
| 0.0021129 | 2 | 1671 | 58,274 | 47,348 | 4 | 0.48042 |
| 0.00011073 | 1 | 17054 | 63,925 | 39,718 | 3 | 0.47343 |
| 4.11E-04 | 2 | 16830 | 82,942 | 82,942 | 3 | NaN |
| 0.0030549 | 1 | 15804 | 47.05 | 27,121 | 3 | 0.61585 |
| 1.02E-08 | 2 | 18995 | 75,416 | 53,565 | 2 | 0.1746 |
| 1.27E-08 | 1 | 22592 | 73,603 | 49.58 | 2 | 0.30054 |
| 4.02E-02 | 2 | 18880 | 57,629 | 41,819 | 2 | 0.2115 |
| 0.0025483 | 1 | 13644 | 47,548 | 16.41 | 4 | 0.5026 |
| 0.0068367 | 1 | 20960 | 42,314 | 13,982 | 4 | 0.32278 |
| 0.0070169 | 1 | 20592 | 42,095 | 26,493 | 4 | 0.57424 |

| Ratio H/L normalized | Ratio H/L shift | Intensity | Intensity L | Intensity H | Reverse | Potential contaminant |
|---|---|---|---|---|---|---|
| 0.57984 | 0 | 119240 | 84688 | 34548 | | |
| 0.73098 | 0 | 88880 | 65772 | 23108 | | |
| 0.35155 | 0 | 247460 | 209250 | 38214 | | |
| 0.53892 | 0 | 229620 | 176360 | 53258 | | |
| 0.51506 | 0 | 164080 | 137950 | 26132 | | |
| 0.28614 | 0 | 192690 | 172720 | 19962 | | |
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| 0.65471 | 0 | 401910 | 277420 | 124490 | | |
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| 10,078 | 0 | 359240 | 234560 | 124680 | | |
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| 13,431 | 0 | 273570 | 164130 | 109440 | | |
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| 0.21051 | 0 | 289450 | 271610 | 17837 | | |
| 0.15605 | 0 | 231540 | 220620 | 10918 | | |
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| 0.57834 | 0 | 215610 | 156630 | 58975 |
| 0.29314 | 0 | 165720 | 146660 | 19056 |
| 0.11562 | 0 | 61337 | 54770 | 6566.9 |
| 0.78028 | 0 | 309790 | 261000 | 48791 |
| 0.67052 | 0 | 567380 | 403460 | 163920 |
| 1,057 | 0 | 122240 | 78061 | 44174 |
| 0.76923 | 0 | 259970 | 200520 | 59452 |
| 10,578 | 0 | 255800 | 185350 | 70457 |
| 0.37952 | 0 | 90624 | 68113 | 22511 |
| 0.68932 | 0 | 1099700 | 782150 | 317510 |
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| 0.47149 | 0 | 1000500 | 723220 | 277270 |
| 0.38078 | 0 | 175680 | 126400 | 49279 |
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| 0.92394 | 0 | 245390 | 165200 | 80189 |
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| 0.67576 | 0 | 1507900 | 1142600 | 365350 |
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| 1,205 | 0 | 249100 | 134730 | 114360 |
| 0.71817 | 0 | 101870 | 78338 | 23527 |
| 0.29435 | 0 | 222970 | 194040 | 28930 |
| 0.44968 | 0 | 563920 | 450140 | 113770 |
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| 0.38264 | 0 | 677870 | 528810 | 149060 |
| 1,103 | 0 | 233860 | 170080 | 63786 |
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| 0.42529 | 0 | 224170 | 173460 | 50716 |
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| 23,934 | 0 | 141910 | 51627 | 90278 |
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| 0.36563 | 0 | 1630400 | 1123800 | 506620 |
| 0.32395 | 0 | 109120 | 94661 | 14462 |
| 0.8344 | 0 | 107580 | 74859 | 32725 |
| 0.83063 | 0 | 70607 | 51988 | 18619 |
| 1,167 | 0 | 85966 | 59484 | 26482 |
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| 0.77457 | 0 | 121610 | 85316 | 36293 | |
| 0.74515 | 0 | 86893 | 58523 | 28370 | |
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| 0.57051 | 0 | 169540 | 106950 | 62587 | |

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| 0.030196 | 0 | 1422400 | 1411100 | 11342 |
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| 0.1905 | 0 | 91803 | 87186 | 4617 |
| 0.25369 | 0 | 133890 | 120940 | 12953 |
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| 0.72339 | 0 | 124750 | 78014 | 46734 |
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| 0.42596 | 0 | 64606 | 42323 | 22282 |
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| 10,295 | 0 | 296540 | 200440 | 96097 |
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| 11,492 | 0 | 5734100 | 3887800 | 1846300 |
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| 0.45734 | 0 | 108830 | 63209 | 45622 |
| 0.64593 | 0 | 75413 | 67108 | 8304.4 |
| 18,009 | 0 | 78514 | 40108 | 38407 |
| 0.68216 | 0 | 64185 | 49273 | 14912 |
| 0.62224 | 0 | 64049 | 44530 | 19519 |
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| 0.29914 | 0 | 55770 | 45824 | 9946.3 |
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| 0.592 | 0 | 448200 | 395640 | 52557 |
| 0.4054 | 0 | 333960 | 290510 | 43447 |
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| id | Protein group IDs | Peptide ID | Mod. peptide ID | MS/MS IDs | Best MS/MS | AIF MS/MS IDs |
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| 155 | 716 | 11 | 15 | 235 | 235 | |
| 156 | 716 | 11 | 15 | 236 | 236 | |
| 157 | 716 | 11 | 16 | 237 | 237 | |
| 158 | 716 | 11 | 16 | 238 | 238 | |
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| 4067 | 1087 | 423 | 492 | 6632 | 6632 | |
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| 5844 | 134 | 609 | 717 | 9553 | 9553 | |
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| 5846 | 134 | 609 | 717 | 9555 | 9555 | |
| 5847 | 134 | 609 | 717 | 9556 | 9556 | |

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| 6912 | 147 | 734 | 861 | 11389 | 11389 |
| 6913 | 147 | 734 | 861 | 11390 | 11390 |
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| 17924 | 1852 | 2030 | 2313 | 29692 | 29692 |
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| 35810 | 731 | 4226 | 4736 | 59386 | 59386 |
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| 51752 | 1339 | 6224 | 7022 | 85315 | 85315 |
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| 55318 | 42 | 6674 | 7597 | 90819 | 90819 |
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| 57336 | 1374 | 6907 | 7934 | | |

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| 58607 | 1959 | 7058 | 8144 | 95986;95987 | 95987 |
| 58608 | 1959 | 7058 | 8144 | 95988 | 95988 |

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| 58801 | 73 | 7093 | 8180 | | |

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| 60063 | 1276;1814;13 | 7314 | 8414 | 98100 | 98100 |
| 60064 | 1276;1814;13 | 7314 | 8414 | 98101;98102 | 98102 |

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